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RESULT ADMILIT ADMILITATION AND ADMI
STRÀIN-C57BL/65; TISSUE-Heart;
MADLING-21085660; PubMed-11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Kadota K., Matsuda H.A., Ashburner M., Pesole G., Quackenbush
Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush
Schriml L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Adipocyte;

MEDLINE-96070757; PubMed-7592907;

MEDLINE-96070757; PubMed-7592907;

Scherer P.E., Williams S., Fogliano M., Baldini G., Lodish H.F.;

Scherer P.E., Williams S., Fogliano M., Baldini G., Lodish H.F.;
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Q60994; Q62400; Q90C68;
Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Adiponectin precursor (30 kDa adipocyte complement-related protein)
(ACRP30) (Adipocyte specific protein AdipoQ).
APMI OR ACRP30 OR ADIPOQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      Blochem. Blophys. Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=11162643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96209999; PubMed=8631877;
Hu E., Liang P., Spiegelman B.M.;
"AdipoQ is a novel adipose-specific gene dysregulated in obesity.";
J. Biol. Chem. 271:10697-10703(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Rodentia;
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         EMBL; U37222; AAA80543.1; -.
EMBL; U49915; AAB06706.1; -.
EMBL; AR304466; AAK13417.1; -.
EMBL; AK003138; BAB22597.1; -.
MGD; MGT:106675; Acrp30.
InterPro; IPR001073; C19.
InterPro; IPR000087; Collagen.
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                                                                                                                                                                                                                                                                                        Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen;
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Hormone; Collagen; Signa
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SMART; SM00110; C1Q; 1.
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                                                                                                                                                                                Polymorphism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . Med. 7:947-953(2001).

FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMMATORY RESPONSES THROUGH ITS INHIBITORY FUNCTIONS. INHIBITS ENDOTHELIAL NF-KAPPAB SIGNALING THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS TNF-ALPHA-INDUCED EXPRESSION OF ENDOTHELIAL ADHESION MOLECULES. INVOLVED IN THE CONTROL OF FAT METABOLISM AND INSULIN SENSITIVITY.

SUBGUIT: HOMOOLIGOMER.
SUBGUIT: HOMOOLIGOMER.
SUBGULTULAR LOCATION: SECRETED IN PLASMA.

TISSUE SPECIFICITY: SYNTHESIZED EXCLUSIVELY BY ADIPOCYTES AND SECRETED INTO SERUM.
INDUCTION: DURING HORMONE-INDUCED ADIPOSE DIFFERENTIATION AND NEGROUS AND SECRETED INTO SERUM.
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SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN
SIMILARITY: CONTAINS 1 C1Q DOMAIN.
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adipocyte-secreted
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d protein Acrp30 enhances
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                    ADIPONECTIN.
COLLAGEN-LIKE.
C10.
INTERCHAIN (BY:
HYDROXYLATION (I
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L., Kagechika
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 C10B_MOUSE
C1QA_HUMAN
C1QA_MOUSE
GLIC_MOUSE
GLIE_HUMAN
HP25_TAMSI
HP27_TAMSI
CQT3_HUMAN
HP20_TAMSI
CQT1_HUMAN
CQT1_HUMAN
CA13_BOVIN
CA13_RAT
CA13_NOUSE
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APMI_HUMAN
APMI_HUMAN
CA1A_HUMAN
CA1A_CHICK
C10C_MOUSE
CA1A_BOVIN
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CA1A_MOUSE
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APM1 OR ACRP30 OR GBP28.
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adiponectin
                                                                                                       Saito K., Tobe T., Minoshima S., Asakawa
Nakano Y., Shimizu N., Tomita M.;
"Organization of the gene for gelatin-bir
                                                                                                                                                                                                                                                                                                                 MEDLINE-96224171; PubMed-8619847;
                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=99196984; PubMed=10095105;
                                                                                                                                                                                                                                                                           Matsubara K.;
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                                                                                                                                                                                                                           "CONA cloning and expression of a novel adipose Specific factor, apmi (Adipose Most abundant Gene transcript 1)."; Biochem. Biophys. Res. Commun. 221:286-289(1996).
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                 SEQUENCE FROM N.A.
MEDLINE-99333693; PubMed-10403784;
Schaeffler A., Orso E., Palitzsch
Schaeffler A., Orso E., Schait
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precursor (30 kDa adipocyte complement (apM-1) (Gelatin-
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                                                                                                                        (GBP28).";
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RA HATA K., BOUTIN P., MORI Y., TODE K., DINA C., YASUDA K., YAMAUCHI T., RA OTADE S., OKADA T., ETO K., KADOWAKI H., Hagura R., AKANUMA Y., RA OTADE S., OKADA T., ETO K., KADOWAKI H., Hagura R., AKANUMA Y., RA YAZAKI Y., NAGAI R., TANIYAMA M., MATEUBARA K., YODA M., NAKANUMA Y., RA YAZAKI Y., NAGAI R., TANIYAMA M., MATEUBARA K., YODA M., NAKANUMY., RA YAZAKI Y., NAGAI R., TANIYAMA M., MATEUBARA K., YODA M., NAKANUMY., RA YAZAKI Y., NAGAI R., TANIYAMA M., KIMURA S., ITO C., FROGUEL P., KADOWAKI T., RT ANI RECORD THE S., TOMITA S., ITO C., FROGUEL Y., KADOWAKI T., RT ANI YAZAKI Y., NAGAI Y., NAGAI Y., RA YAZAKI Y., NAGAI Y., NAGAI Y., RA YAZAKI Y., NAGAI Y., NAGAI Y., NAGAI Y., NAGAI Y., NAGAI Y., RA YAZAKI Y., RA YAZAKI Y., NAGAI YAZAKI YAZAKI Y., NAGAI YAZAKI YAZAKI Y., NAGAI YAZAKI YAZAKI YAZ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       negatively regulates the growth of functions of macrophages."; Blood 96:1723-1732(2000).
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MEDLINE-20417747; PubMed-10961870;
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Akanuma Y., Gavrilova O., Vins
Shudo K., Yoda M., Nakano Y.,
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Horie M., Shimomura I., Hotta K., Kuriyama H., Kihara
Yamashita S., Funahashi T., Matsuzawa Y.;
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T., Kamon J., Waki H., Tsuboyama-Kasaoka N., Ezaki O.,
Y., Gavrilova O., Vinson C., Reltman M.L., Kagechika H.,
Y.Oda M., Nakano Y., Tobe K., Nagai R., Kimura S., Tomi
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Kihara S., Funahashi T., Tenner
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16-OCT-2001
                                                                                                                                      MEDLINE-97255959; PubMed-9101290;
Kuivanlemi H., Tromp G., Prockop D.J.;
"Mutations in fibrillar collagens (types I, II, III, and XI), fibril-
associated collagen (type IX), and network forming collagen (type X)
cause a spectrum of diseases of bone, cartilage, and blood vessels.";
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                        MEDLINE-94136476; PubMed-8304336; Wallis G.A., Rash B., Sweetman W.A.,
                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 547-655 FROM N.A. MEDLING=92077285; PubMed=1743401; Reichenberger E., Aigner T., von "In situ hybridization studies on in fetal human cartilage.";
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Beler F., Lammi M.B.,
Submitted (JUN-1996)
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Apte S.S., Seldin M.F., Hayashi M
"Cloning of the human and mouse t
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MEDLINE=93012005; PubMed=1397333;
Reichenberger E., Beier F., Luvalle
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MEDLINE-9210955; PubMed-1764025;

Thomas J.T., Cresswell C.J., Rash B., Nicolai H.,

Solomon E., Grant M.E., Boot-Handford R.P.;
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pha 1(X) chain precursor.
    Boot-Handford
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human and mouse type X collage
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206:217-224(1992).
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McIntosh I., Abbott M.H., Warman M.L., Olsen B.R., Francomano C.A.; *Additional mutations of type X collagen confirm COL10A1 as the schmid metaphyseal chondrodysplasia locus."; Hum. Mol. Genet. 3:303-307(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *Amino acid substitutions of conserved residues in the carboxyl-terminal domain of the alpha 1(X) chain of type X collagen occur in two unrelated families with metaphyseal chondrodysplasia
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Bonaventure J., Chaminade F., Maroteaux P.;
"Mutations in three subdomains of the carboxy-terminal region
collagen type X account for most of the Schmid metaphyseal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chan D., Cole W.G., Rogers J.G., Bateman J.F.;
"Type x collagen multimer assembly in vitro is prevente
to Val mutation in the alpha 1(X) NCl domain resulting
metaphyseal chondrodysplasia.";
J. Biol. Chem. 270:4558-4562(1995).
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"Mutations within the gene encoding the alpha 1 (X) chain of type collagen (COL10A1) cause metaphyseal chondrodysplasia type Schmid not several other forms of metaphyseal chondrodysplasia.";
J. Med. Genet. 33:450-457(1996).
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Sawai H., Ida A., Nakata Y., Koyama K.;

Novel missense mutation resulting in the substitution of tyrosine cysteine at codon 597 of the type X collagen gene associated with schmid metaphyseal chondrodysplasia.";

J. Hum. Genet. 43:259-261(1998).

I. Hum. Genet. 43:259-261(1998).

I. FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE MINERALIZATION ZONES OF HYALINE CARTILAGE.
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Am. J. Hum. Genet.
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Hum. Mutat. 9:131-135(1997).
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MEDLINE=97220591; PubMed=9067753;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS SMCD ARG-545; GLU-595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94272470; PubMed-8004099;
                                                                                                                                                                                                                                                                                                                                                                                                      "Mutation of the type X collagen gene spondylometaphyseal dysplasia."; Am. J. Hum. Genet. 63:1659-1662(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99057503; PubMed-9837818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Mutations in the N-terminal globul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS SMD GLU-595
                                                                                                                                                                                                                                                                                                                                              VARIANT SMCD CYS-597.
MEDLINE-99069781; PubMed-9852679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakamura Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ikegawa S., Nishimura
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SUBUNIT: HOMOTENMER.

SUBUNIT: HOMOTENMER.

UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OF ALL OF THE CHAINS.

DISCASE: DEFECTS IN COLIDAL ARE THE CAUSE OF SCHMID TYPE

METAPHYSEAL CHONDRODYSPLASIA (SMCD), A DOMINANTLY INHERITED

DISCARDER OF THE OSSEOUS SKELETON. THE CARDINAL FEATURES OF THE

PHENOTYPE ARE MILD SHORT STATURE, COXA VARA AND A WADDLING GAIT.

PHENOTYPE ARE MILD SHORT STATURE, COXA VARA AND A WADDLING GAIT.

RADIOGRAPHY USUALLY SHOWS SCLEROSIS OF THE RIBS, FLARING OF THE

RADIOGRAPHY USUALLY SHOWS SCLEROSIS OF THE RIBS, ESPECIALLY OF THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G., Nagai T., Hasegawa T., Ohashi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ano A., Haga N., Nakamura Y.;
globular domain of the type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIS-597;
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Pfam; PF01391; Collagen; 8.
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DISEASE: DEFECTS
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SKELETAL DYSPLASIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; AL121963; CAB87590.1; -...; S68531; AAC60615.1; -...; X58879; CAA41686.1; -...; X74050; AAA6122.1; -...; X72599; CAA51170.1; JOIN
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                          461 GFPGSKGDPGSPGPPGPAGIATKGLNGPTGPPGPPGPRGHSGEPGLPGPPGPPGPPGQAV
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                                                                                                               Similarity 34.9
98; Conservative
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                                                                     GNPGLPGPKGDPGVGGPPGLPGPVGPAGAKGMPGHNGEAGPRGAPGIPGTRGPIGPPGIP
                                                                                         GSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLP
       VP-
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                                                                                                                                                                                                                                             NONHELICAL
C1Q.
                                                                                                                          Score 418.5;
Pred. No. 3.
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C -> R (IN SMCD)
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                                                                                                                                                                                                                                                                                                   POTENTIAL.
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G -> R (IN SMCD)
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CANA_CHICK

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CANA_CHICK

COP0125;

DT 01_AGC-1988 (Rel. 08, Created)

DT 01_AGC-1989 (Rel. 20, Last sequence update)

DT 01_AUG-1999 (Rel. 30, Last sequence update)

DE COL10A1

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OS GAILUS (ALSCO)

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OS GAILUS (ALSCO)

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OS RACIL_TAXID-9031;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamaguchi N., Benya P.D., van der Rest M., Ninomiya Y.;
"The cloning and sequencing of alpha l(VIII) collagen cDNAs demonstrate that type VIII collagen is a short chain collagen and contains triple-helical and carboxyl-terminal non-triple-helical domains similar to those of type X collagen.";
J. Biol. Chem. 264:16022-16029(1989)
-I- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYDERTHROPHIC CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE MINERALIZATION ZONES OF HYALINE CARTILAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                      use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentitles requires a license agreement (See http://www.isb-slb.or send an email to license@isb-slb.ch).
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PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-x-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.

SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collable the Swiss Institute of Bioinformatics and the EMBL outsi European Bioinformatics Institute. There are no restrictions
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DOMAIN
                   MEDLINE=96186528; PubMed=8606057; Petry F., McClive P.J., Botto M., Morl The mouse C1q genes are clustered on conservation of gene organization."; Immunogenetics 43:370-376(1996).
                                                                                                                                                                                                                           Petry F., Reid K.B.M., Loos M.;
"Isolation, sequence analysis and characterization of cDNA clones coding for the C chain of mouse Clq. Sequence similarity of complement subcomponent Clq, collagen type VIII and type X and
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complement Clq subcomponent, C chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q02105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Extracellular matrix; Connective tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS;
                                                                                                                            STRAIN-BALB/c;
                                                                                                                                                                                                            precerebellin.";
                                                                                                                                                                                                                                                                                                          STRAIN-ICR; TISSU
MEDLINE-93011118;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ClQG OR ClQC.
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQC_MOUSE
    FUNCTION: C10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF01391; Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; PR00007; COMPLEMNTC10; SM00110; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                        Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIPGLYYFSYHVHAKGTNVWVALYKNGSPVMYTYDEYQKGYLDQA--SGSAVIDLMENDQ
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                                                                                                                          TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                        209:129-134(1992)
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    ASSOCIATES
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
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      HIIM
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                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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      THE
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                                                                ley B.J., Mc
chromosome
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      PROENZYMES
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Matches 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR001073; Clq.
Interpro; IPR000087; Collagen.
Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complement pathway; Plasma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN. SIMILARITY: CONTAINS 1 C1Q DOMAIN.
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x92960; CAA63535.1;
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172 GESIASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFL
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                                                                                                                                                                                                                  Similarity
                                                                                                           APGEKGEGGRPGLPGPRGDPGPRGEA----GPAGPTGPAGECSVPPR------SAFSAKRS
                                                                                                                                                                      LLVLLLLGLAAGSPPLDDNKIPSLC---PGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
                                      TTQY-PEANALVRENSVVTNPQGHYNPSTGKETCEVPGLYYF-VYYTSHTANLCVHLNLN
                                                    ESRVPPPSDAPLPFDRYLVNEQGHYDAVTGKFTCQVPGYYYFAVHATYYRASLQFDLYKN
                                                                                                                                              LLLLFLLAL----PL-RSQASAGCYGIPGMPGMPGAPGKDGHDGLQGPKGEPGIPAVPG
                                                                                           TQGPKGQKGEPGMPGHRGKNGPRGTSGLPGDPGPRGPPGEPGVEGRYKQKHQSVFTVTRQ
                                                                                                                                                                                                                                                           246 AA;
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hes 84;
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                                                                                                                                                                                                                                  Length 246
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P23206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COLLAGEN genes.";
Blochem. J. 273:141-148(1991).
FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC CHONDROTOCITES AND HAS BEEN LOCALIZED TO PRESUMPTIVE CHONDROTOCITES AND HAS BEEN LOCALIZED TO PRESUMPTIVE CHONDROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
Bovidae; Bovinae; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thomas J.T., Kwan A.P.L., Grant M.E., Boot-Handford R.P.; "Isolation of cDNAs encoding the complete sequence of bovine tollagen. Evidence for the condensed nature of mammalian type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91113131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Cartilage;
                                                                                                                                                                                                                                                     CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S13301; S13301.
InterPro; IPR001073; Clq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X53556; CAA37624.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00007; COMPLEMNTC10.
ProDom; PD000007; Collagen; 1.
                                                                                                                  MOD_RES
                                                                                                                                                                                                                                                                                                                                                Extracellular matrix; Connective
                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                  SEQUENCE
                                                                                               CARBOHYD
                                                                                                                                                               DISULFID
                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAIL SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HOMOTRIMER.

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING POINT OR ALL OF THE CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MINERALIZATION ZONES OF HYALINE CARTILAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187
                                                                                                                                                                                                                                                                                                                                                                                             SM00110;
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(Rel. 38, Last annotation
                                                                                                                                                                                                                                                                                                                             Collagen;
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                                                                                                                                                                                                                                                                                                                                                                      C1Q; 1.
13; C1Q;
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519
674
674
197
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       31.18;
                                                                                                                                                                                                                                                                                                                           Signal;
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                                                                                                                                                                                                                                                                                                                               tive tissue; Repeat; Hydroxylation; Glycoprotein.
           Score
Pred.
                                                                                                                                                                                          CIQ.
                                                                                                                                                                                                                                                          COLLAGEN ALPHA 1(X) CHAINONHELICAL REGION (NC2).
                                                                                                                                                                                                                  TRIPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
                                                                                                    N-LINKED
                                                                                                                    HYDROXYLATION
                                                                                                                                                 HYDROXYLATION
                                                                            CD4CA73A03E004CA CRC64;
                                                                                                                                                                       SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
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No.
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                                                                                                    (GLCNAC
              .5; DB 1;
1.1e-21;
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                                                                                                                       78)
78)
                                                                                                                         SIMILARITY).
                                   Length 674;
                                                                                                           (POTENTIAL).
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S 밁 Ş В á В δÃ 밁

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EMBL; AR329839; AAK17963.1; -
EMBL; BC022187; AAH22187.1; -
Genew; HGNC:14342; C10TNE7;
InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
Pfam; PF00386; C1q; 1
Pfam; PF01391; Collagen; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
               DOMAIN
                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
COmplement-clq tumor necrosis factor-related |
ClqTNF7 OR CTRP7.
                                                                               Collagen;
                                                                                                    PRINTS; PRO0007; COM
SMART; SM00110; C10;
                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                         PROSITE; PS01113; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                               SUBBLITEE (JAN-2002) to the EMBL/GenBank/DDBJ databases -- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN. -- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2002) to
                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9BXJ2;
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                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CQT7_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                         iddington C.S., Sheppard P.O.,
Homo sapiens complement-clq tur
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141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                  COMPLEMNTC1Q
              139
276
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289
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           POTENTIAL.
COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
RELATED PROTEIN 7.
COLLAGEN-LIKE.
C1Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lasser G.W.;
s factor-related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein.";
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       RESULT 9
CA1A_MOUSE
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Best Local
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 Elima K., Metsaeranta M., Kallio J.,
Garofalo S., de Crombrugghe B., Vuori
"Specific hybridization probes for mo
                                                                                         Apte S.S., Seldin M.F., Hayashi M., Olsen B.R., "Cloning of the human and mouse type X collagen the mouse type X collagen gene to chromosome 10. Eur. J. Biochem. 206:217-224(1992).
                                                                                                                                                                                                                                           STRAIM-129/Sv; TISSUE-Liver; MEDLINE-93238750; PubMed-8477738; Kong R.Y.C., Kwan K.M., Lau E.T., Grant M.E., Cheah K.S.E.;
                                                        SEQUENCE OF 385-627 FROM N.A. STRAIN-C57BL/6;
                                                                                                                                     MEDLINE=92267014; PubMed=1587271; Apte S.S., Seldin M.F., Hayashi M.,
                                                                                                                                                                                                                                                                                                                          structure and expression pattern.";
Biochem. J. 289:247-253(1993).
                                                                                                                                                               STRAIN-DBA/2J;
                                                                                                                                                                                                                                                                                                                                                                 Elima K., Eerola I., Rosati R
de Crombrugghe B., Vuorio E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence up
01-NOV-1995 (Rel. 32, Last annotation
                                          WEDLINE=92182017; PubMed=1543751;
                                                                                                                                                                            SEQUENCE OF 51-680 FROM N.A.
                                                                                                                                                                                                    'Intron-exon structure, alternative use the mouse collagen x gene, Coll0a-1."; Biochem. 213:99-111(1993).
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93143676; PubMed=8424763; Elima K., Eerola I., Rosati R., M
                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BALB/C
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collagen alpha i(x) chain COL10A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q05306;
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CALA_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GESTASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIK-TDSTFSGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSY--PEERLPIIFNKVLENEGEHYNPATGKFICAFPGIYYFSYDITLANKHLAIGLVHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DQGETGKKGPIGPEGEKGEVGPIGPPGPKGDRGEQGDPGLPGVCRCGSIVLKSAFSVGIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPSL--CPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGGRPGLPGPRGDPGPRGEAGPAGPTGPAGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ã,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                precursor.
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                                                                                                                                                                                                                                                                                                                                                                              R., Metsaranta M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 410.5;
Pred. No. 5.4e
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A61609FF86D26946 CRC64;
               Vuorio
                                                                                                                                                                                                                                                      Thomas J.T., Boot-Handford
                          Peraelae M., Eerola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update
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  alpha
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                                                                                                                                                                                                                              promoter and
2(IX) and alpha 1(X)
                                                                                                                                                                                                                                                                                                                                                                              Garofalo S.,
                                                                                                          genes
                                                                                                                                                                                                                                                                                                                                                    sequence,
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                                                                                                                  and mapping
                                                                                                                                                                                                                            expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---GAPGEKG
                                                                                                                                                                                                                                                                                                                                                                              Perala
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Best Local S
Matches 99
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Blochim. Blophys.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                               CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X67348; CAA47763.1; -. EMBL; X65121; CAA46237.1; -. EMBL; X63013; CAA44741.1; -. EMBL; Z21610; CAA79736.1; -.
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                                                                                                                                                                                                                                                                        CONFLICT
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00386; C1q; 1. Pfam; PF01391; Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: STRONG, TO ALPHA 1 AND
-!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00007; COMPLEMNTC1Q. ProDom; PD000007; Collagen; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01113; C1Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE MINERALIZATION ZONES OF HYALINE CARTILAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-x-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. SIMILARITY: STRONG, TO ALPHA I AND 2 TYPE VIII COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HOMOTRIMER.
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S31216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI:88445;
                                          506
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                                                                                                                                                        392 GEPGLNGPK-----GNPGLPGQKGDPGVGGTPGLRGPVGPVGAKGVPGHNGEAGPRGEP
             118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM00110;
                                                                     87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                   99;
                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                     GSPPLDDNKIPSLCPGHPGLP-----
          PSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNG-ESIA
                                                                                                GIPGTRGPTGPPGVPGFPGSKGDPGNPGAPGPAGIATKGLNGPTGPPGPPGPRGHSGEPG
                                                                                                                             GLPGRDGRDGAPGAPGEKGEGGRPGLPGPR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000087; Collagen.
                                        LPGPPGPPGPPGQAVMPDGFIKAGQRPRLSGMPLVSANHGVTGMPVSAFTVILSKAY--P
                                                                     --GPAGPTGPAGECSVP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001073; C1q
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                                                                                                                                                                                                                                                                         520
545
248
286
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417
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635
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306
417
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                                                                                                                                                                                                                                                                              66775 MW;
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                                                                                                                                                                                                                                30.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    CIQ.
                                                                                                                                                                                                                                Score 408; DB 1;
Pred. No. 1.9e-21;
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NONHELICAL REGION (NC1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NONHELICAL
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                                                                                                                                                                                                                                                                              FE984CA99AF708E2 CRC64;
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                                                                         PRSAFSAKRSESRVPP
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RESULT 10
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IS JUMAN
DT 15-JUM
DX MARMINAL
RN [1]
RN [2]
RN [2]
RN SEQUEN
RA STRAW
SUBMIT
CC -1- S:
CC This:
CC This:
CC This:
CC This
CC This
RM SUBMIT
DR EMBL;
DR EMBL;
DR EMBL;
DR EMBL;
DR FAIN
DR PRINT
DR
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          piddington C.S., Bishop P.;
"Homo sapiens complement-clq tumor necrosis factor-related protein.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CQT2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ω9ВХJ5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L5-JUN-2002 (Rel. 41, Last sequence ulles-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:14325; C1QTNF2.
InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF329836; AAK17960.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01113; C10;
                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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PF01391; Collagen;
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              109
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                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                           LLGLAA-----GSPPLDDNKIPSLC------PGHPGLPGTPGHHGSQGLPGRDGRDG 54
                                                        HDGDRGDSGEEGPPGRTGNRGKPGPKGKAGAIGRAGPRGPKGVNGTPGKHGTPGKKGPKG 130
                                                                                                                                               LLGAFARRDERKGSPQL-----VCSLPGPQGPPGPPGAPGPSGMMGRMGFPGKDGQDG
              KRSESRVPPPSDA---
                                                                                                  RDGAPGAPGEKGEGGRP---GLPGPRGDPGPRGEAGPAGP---TGPAGECSVPPRSAFSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal.
                                                                                                                                                                                                                                                                                                                               40
143
285 AA;
                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C10;
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285 C
29952 MW;
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                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                            Score 403; DB 1; Pred. No. 1.8e-21; Pred. No. 1.8e-21; Prematches 91;
                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.

COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
RELATED PROTEIN 2.

COLLAGEN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                             C10
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                  PLPFDRVLVNEQGHYDAVTGKFTCQ 146
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                                                                                                                                                                                                                                                                                              Length 285;
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RESULT 11
              P02747; Q96DL2; Q96H05;
21-JUL-1986 (Rel. 01, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hata H., Nakagawa S., Senoh A., Mizuguchi H., Inaga
Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamu
Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa
Kawakami B., Nagai K., Isogai T., Sugano S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization and organization of the genes encoding the A-, and C-chains of human complement subcomponent Clq. The complete derived amino acid sequence of human Clq.";
Biochem. J. 274:481-490(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Monocytes;
MEDLINE=91174759; PubMed=1706597;
Sellar G.C., Blake D.J., Reld K.B.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complement Clq subcomponent, C chain precursor.
                                                                                                                                                                                                                                                                            Petry F.
                                                                                                                                                                                                                                                                                          REVIEW OF C1Q DEFICIENCY.
MEDLINE=98450587; PubMed=9777412;
                                                                                                                                                                                                                                                                                                                                                                                   *Complete amino acid sequences of the three collagen-like regions present in subcomponent Clq of the first component of human
                                                                                                                                                                                                                                                                                                                                                                                                                                  {4}
SEQUENCE OF 29-122.
Sequence of 29-122.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
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                                                                                                                                                                                                                                                                                                                                                   Biochem. J. 179:367-371(1979).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'NEDO human
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  PTM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an cDNA sequencing project."; (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MAY-2001) to the EMBL/GenBank/DDBJ databases
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, Kawamura M.,
shikawa T., Sug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suzuki Y.,
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Matches Query Match Best Local

100;

Conservative

33; Score Pred.

Mismatches 397; DB 1 No. 4e-21;

84;

Gaps

57

1;

Length 245 Indels 34;

Similarity

30.0%;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                              Repeat; Signal;
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:1245; C1QG.
MIM; 120575; -.
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                                                                                                 VARIANT
                                                                                                                                    MOD_RES
                                                                                                                                               CARBOHYL
                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000087;
                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001073; Clq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISEASE: DEFECTS IN C10G ARE A CAUSE OF C10 DEFICIENCY. IT IS RARE GENETIC DISORDER WHICH IS ASSOCIATED WITH RECURRENT INFECTIONS AND A HIGH PREVALENCE OF LUPUS ENTHEMATOSUS-LIKE SYMPTOMS. IT IS CHARACTERIZED BY A LOSS OF ACTIVATION OF THE COMPLEMENT CLASSICAL PATHWAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ween the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN. SIMILARITY: CONTAINS 1 C1Q DOMAIN.
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S14351; S14351.
                                                                                                                                                                                                                                                                                                                               pathway; Plasma; Hydroxylation; Glycoprotein; Collagen;
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                                                                                                                                                                                                                                                                                                                        Disease mutation.
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25774 MW;
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HYDROXYLATION.
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G -> R (IN C10
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                                                                                                                                                                                                              HYDROXYLATION.
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CRC64;
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                                                                                                            EMBL; J05042; AAA31204.1; --
PIR; A34246; A34246.
InterPro; IPR0001073; C1q.
InterPro; IPR000087; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Collagen alpha 1(VIII) chain precursor (Endothelial collagen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RABIT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA18_RABIT
                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.lsb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                           -I- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

-I- MISCELLANEOUS: FOUR CONSECUTIVE GLY-PRO-PRO TRIPLETS ARE PRESENT AT THE C-TERMINUS OF THE TRIPLE-HELICAL RECION. THESE MAY PROVIDE HIGH THERMAL STABILITY OF THIS REGION OF THIS REGION.

-I- SIMILARITY: STRONG, TO ALPHA 2 TYPES VIII AND X COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamaquchi N., Benya P.D., van der Rest M., Ninomiya Y.;
"The cloning and sequencing of alpha 1(VIII) collagen cONAs
demonstrate that type VIII collagen is a short chain collagen and
contains triple-helical and carboxyl-terminal non-triple-helical
domains similar to those of type X collagen.";
J. Biol. Chem. 264:16022-16029(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vercebraca; Eu
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9986;
 Glycoprotein;
SIGNAL
   Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Cell adhesion; Collagen; Signal.

1 20
                                                          PROSITE; PS01113; C1Q;
                                                                       PRINTS; PRO0007; COMPLEMNTC1Q. SMART; SM00110; C1Q; 1.
                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: MAJOR COMPONENT OF THE DESCEMET'S MEMBRANE (BASEMENT NEMBRANE) OF CORNEAL ENDOTHELIAL CELLS.
SUBUNIT: MAY FORM HOMOTRIMERS, OR HETEROTRIMERS IN ASSOCIATION
                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 1 C10 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WITH ALPHA 2(VIII) TYPE COLLAGENS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKLLLLLLLPLR------GQANTGCYGIPGMPGLPGAPGKDGYDGLPGPKGEPGIPA
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CCC -1- FT CCC -1- CC CCC -1- 
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Best Local
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p98085; 091080;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Inner ear-specific collagen precursor (Saccular collagen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lepomis macrochirus (Bluegill).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDILINE-95167486; PubMed-7863331;

Davis J.G., Oberholtzer J.C., Burns F.R., Greene M.I.;

Paylis J.G., Oberholtzer J.C., Burns F.R., Greene M.I.;

"Molecular cloning and characterization of an inner ear-specific structural protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Centrarchidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COLE_LEPMA
                                                                                                                                                                                                         -!- TISSUE SPECIFICITY: SPECIALIZED SECRETORY SUPPORTING OUTER PERIMETER OF THE SACCULAR EPITHELIUM.
-!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
-!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHI INTRODUCED FOR POSITIONS 391-419 SO AS TO MAXIMIZE TH WITH OTHER SHORT-CHAIN COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-1995) to the SWISS-PROT data bank.
-!- FUNCTION: FORMS A MICROSTRUCTURAL MATRIX WITHIN THE MEMBRANE (PROBABLY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=13106
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gibson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 267:1031-1034(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONCEPTUAL TRANSLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204
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                                                                                                                                   SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the El
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYDEYKKGFLDQA--SGSAVLLLRPGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CQVPGVYYFAVHATVYRASLQFDLVKNGESIA-SFFQFFGGWPKPASLSGGAMVRLEPED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPSLC--PGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLP-----
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Pred. No. 4.7e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C1Q.
; 2A8CEF1EF8274E99 CRC64;
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NONHELICAL REGION (NC2
TRIPLE-HELICAL REGION.
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MAXIMIZE THE S
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                                                                                                                                                                                                                                                                                                                                                        CELLS AT
                                                                                                                                                    EMBL
                                                                                                                                                                                                                                                  SIMILARITY
                                                                                                                                                    a collaboration - 
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                              THE
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: MAJOR COMPONENT OF THE DESCEMET'S MEMBRANE
MEMBRANE) OF CORNEAL ENDOTHELIAL CELLS.
-I- SUBUNIT: MAY FORM HOMOTRIMERS, OR HETEROTRIMERS IN AS
                                                                                                                                                                                                   CA18_HUMAN STANDARD; PRT; 744 AA. P27658; Q96D07; 01-AUG-1992 (Rel. 23, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) COllagen alpha 1(VIII) chain precursor (Endothelial Collagen alpha 1(VIII) chain precursor (Endothelial Collagen alpha 1(VIII) chain precursor (Endothelial Collagen alpha 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
                                                                                Muragaki Y., Mattel M.-G., Yamaguchi N., Olsen The complete primary structure of the human assignment of its gene (COLBAL) to chromosome Eur. J. Blochem. 197:615-622(1991).
                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-91231001; PubMed-2029894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                    TISSUE-Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0007; COMPLEMNTC1Q. SMART; SM00110; C1Q; 1. PROSITE; PS01113; C1Q; 1.
                                                               SEQUENCE FROM N.A.
                                                                                                                                                       NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Extracellular matrix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00386; C1q; 1. Pfam; PF01391; Collagen; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U17431; AAA69978.1; ALT_FRAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001073; Clq.
                                                                                                                                                                                                                                                                                                            394
                                                                                                                                                                                                                                                                                                                                                   337
                                                                                                                                                                                                                                                                                                                                                                                                         101 PPRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVY
                                                                                                                                                                                                                                                                                                                                                                      161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 GEPGLNGTKGSIGREGPMGPGLAGTKGLKGEQGLKGECLQGEKGERGPPGLRGEMGLNGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 GSPPLDDNK--IPSLCPGHPGLPGTPGHHGSQGLPGR--DGRDGRDGAPGAPGEKGEGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 PGLPGPRGDPGP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
96; Conserv
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                                                                                                                                                                                                                                                                                                           SSEDDSTFSGFLLYPD
                                                                                                                                                                                                                                                                                                                            SIKTDSTFSGFLVYSD
                                                                                                                                                                                                                                                                                                                                                NRPVRAALVVNGVRKLRTRDSLYGQDIDQA--SNLALLHLTDGDQVWLET-LRDWNGXYS
                                                                                                                                                                                                                                                                                                                                                                                        QIRSAFSVGLFPSRSFPPPSLPVKFDKVFYNGEGHWDPTLNKFNVTYPGVYLFSYHITVR
                                                                                                                                                                                                                                                                                                                                                                                                                               DGVKGERGEPGPLGGKGDTGARGPPGPPGGRGMAGLRGEKGLKGVRGPRGPKGPPGESVE
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419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW.
                                                                                                                                                                                                                                                                                                          409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 373; DB 1; Le
pred. No. 3.1e-19;
"" amatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NONHELICAL REGION (NC1).
(C1Q.
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
; 570CDB9675FC0F39 CRC64;
                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NONHELICAL REGION (NC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INNER EAR-SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collagen; Signal
                                                                                        Olsen B.R., Ninomiya Y.; uman alpha 1 (VIII) chain and osome 3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NC2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 419;
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                                                                                                                                                                                                     collagen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
  ASSOCIATION
                     (BASEMENT
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                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 120251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>:</del>
                             204
                                                                                          595
                                                                                                                                535
                                                                                                             100
                                                                                                                                                    75
         RVFLQMPSEQAAGLYAGQYVHSSFSGYLLY 742
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InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
Pfam; PP00386; C1q; 1.
Pfam; PF01391; Collagen; 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00007; COMPLEMNTC1Q. ProDom; PD000007; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01113; C1Q; Extracellular matrix; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00110; C1Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement
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PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

MISCELLANEOUS: FOUR CONSECUTIVE GLY-PRO-PRO TRIPLETS ARE PRESENT AT THE C-TERMINUS OF THE TRIPLE-HELICAL REGION. THESE MAY PROVIDE THE HIGH THEBWAL STABLILTY OF THIS REGION.

SIMILARITY: STRONG, TO ALPHA 2 TYPES VIII AND X COLLAGENS.

SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 475 VPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGIPGPKGEPGLPGPPGFPGIGK 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:2215; COL8A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                           PGVAGLHGPPGKPGALGPQGQPGLPGPPGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDG
QVWVQVGVGDYIGIYASIKTDSTFSGFLVY 233
                                                                                                                                                                                               VKPPHAYGAKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRQNYNPQTGIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Connective tissue; Repeat; hesion; Collagen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                  -GPRGDPGPRGEAGPAGPTGP----
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P -> L (IN P -> R (IN P -> S (IN P -> T (IN P -> T
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Pred. No. 1.2e-18;
4; Mismatches 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COLLAGEN ALPHA 1(VIII)
NONHELICAL REGION (NC2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGION (NC1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydroxylation;
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RESULT 15
CA18_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RA Arakawa T., Hara A., Fikunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojbori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kidota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kidota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Mynshav-Borls A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
Q00780; Q9D2V4;
01-NOV-1995 (Rel. 32, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       collagen polypeptide and are expressed by various epithelial, endothelial and mesenchymal cells in newborn mouse tissues. "Eur. J. Blochem. 207:895-902(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-C578L/6J; 'MEDLINE-21085660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA18_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
-I- FUNCTION: MAJOR COMPONENT OF THE DESCEMET'S MEMBRANE (BASEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muragaki Y., Shiota C.,
Ninomiya Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92362626; PubMed=1499564;
Muragaki Y., Shiota C., Inoue M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collagen alpha 1(VIII) chain precursor.
            EMBL; x66976; CAA47387.1; -. EMBL; x66977; CAA47387.1; JC EMBL; AK018742; BAB31383.1; PIR; $23779; $23779.
                                                                                                               use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Alpha 1(VIII)-collagen gene transcripts encode a short-chain collagen polypeptide and are expressed by various epithelial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                      WITH ALPHA 2(VIII) TYPE COLLAGENS.
TISSUE SPECIFICITY: HIGH LEVELS IN CALVARIUM,
NEWBORN MICE: ALSO IN VARIOUS EPITHELIAL, ENDO
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEMBRANE) OF CORNEAL ENDOTHELIAL CELLS.
SUBUNIT: MAY FORM HOMOTRIMERS, OR HETEROTRIMERS IN ASSOCIATION
                                                                                                                                                                                                                                                                                                                                                        MESENCHYMAL CELLS.
                                                                                                                                                                                                                                                                                                            PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
                                                       JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ooshima A.,
                                                                                                                                                                                                                                                                                            TYPES VIII AND X COLLAGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              743
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Best Local
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CONFLICT
CONFLICT
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Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Cell adhesion; Collagen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0007; COMPLE
SMART; SM00110; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen;
                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001073; Clq
                                                                                                                                                                                                                                                             CONFLICT
                                         650
                                                             141
                                                                                  590
                                                                                                      104
                     200
 708
                                                                                                                                                                                                                    Similarity
                                                                                  GIDGVKTPHAYAGKKGKHGGPAYEMPAFTAELTVPFPPVGAPVKFDKLLYNGRQNYNPQT
                                                                                                                                       PGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLPGPRGDP-----
                                                             GKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIA-SFFQFFGGWPKPASLSGGAMVRL
                                                                                                                         PGVGKPGVAGLHGPPGKPGALGPQGQPGLPGPPGPPGPPGPPAVMPTPSPQGEYLPDMGL
                                                                                                                                                                 PGLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIVGPSGPIGPPGIPGPKGEPGLPGPPGF
                                         GIFTCEVPGVYYFAYHVHCKGGNVWVALFKNNEPMMYTYDEYKKGFLDQA--SGSAVLLL
RPGDQVFLQMPSEQAAGLYAGQYVHSSFSGYLLY 741
                    EPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVY 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000087;
                                                                                                                                                                                                                                                  743 AA;
                                                                                                                                                                                                                                                                                                                                                        29
118
172
572
                                                                                                                                                                                                                                                                      109
109
248
313
323
361
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ollagen; 7.
COMPLEMNTC1Q.
                                                                                                      SAFSAKR---
                                                                                                                                                                                                                                                                       109
109
248
313
324
361
                                                                                                                                                                                                                                                  719
73454
                                                                                                                                                                                                                   27.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collagen.
                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                                           36;
                                                                                                                                                                                                                                                 IP -> SR (IN REF. 1).
D -> H (IN REF. 1).
T -> P (IN REF. 2).
MPS -> NPF (IN REF. 1).
W; F584D85BD53897F4 CRC64;
                                                                                                     -----SESRVP-PPSDAPLPFDRVLVNEQGHYDAVT
                                                                                                                                                                                                        Score 366.5; DB 1;
Pred. No. 1.5e-18;
6; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                        NONHELICAL REGION (NC1).
                                                                                                                                                                                                                                                                                                                                                                            NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION (COL1).
                                                                                                                                                                                                                                                                                                     P -> L (IN REF. 1).
P -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                 COLLAGEN ALPHA 1(VIII)
                                                                                                                                                                                                                                                                                                                          -> R (IN REF. 2).
-> Y (IN REF. 1).
-> KG (IN REF. 2)
                                                                                                                                                                                                                              Length 743;
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN.
                                                                                                                                                                                                            71;
                                                                                                                                                                                                            Gaps
                                                                199
                                                                                                       140
                                                                                                                            589
                                             707
                                                                                                                                                103
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search completed: June 18, 2003, 14:53:00
Job time : 24 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd

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Result
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Maximum Match 100%
Listing first 45 summaries
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is derived by analysis of the total score distribution.
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seq length: 2000000000
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
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3, Appli
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9, Appli
20, Appli
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24, Appli
294, Appli
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11, Appl
7, Appli
14, Appl
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APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 243
TYPE: PAT
CORGANISM: Homo sapiens
US-09-140-804-2

Score 1325; DB 4; Pred. No. 9.5e-114;

Length 243;

## ALIGNMENTS

US-09-140-804-2

Sequence 2, Application US/09140804 Patent No. 6197930

GENERAL INFORMATION:

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RESULT 2
US-09-336-536-3
; Sequence 3, Application
; Patent No. 6406884
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Best Local Similarity
Matches 243; Conserv
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GENERAL INFORMATION:
APPLICANT: Lelby, K.
APPLICANT: MCKAY, C.
APPLICANT: MCKAY, C.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USIFILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT EILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
NUMBER OF SEQ ID NOS: 75
SOTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 243
TYPE: PRT
ORGANISM: Homo sapiens
US-09-336-536-3
                                                                                                                                                                                                                                         APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cel
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT ELLING DATE: 1998-11-09
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 295
LENGTH: 243
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ORGANISM: Rat
5-09-188-930-295
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Patent No. 615050
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Pred. No. 8.2e-109;
5; Mismatches 7;
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Pred. No. 9.5e-114;
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GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: MCKAY, C.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
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SEQ ID NO 10
LENGTH: 243
TYPE: PRT
                                                                                                                                                        Sequence 4, Application US/09336536 Patent No. 6406884
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOFFILE REFERENCE: 7853-144
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5. 6406884
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Pred. No. 1.3e-107;
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GENERAL INFORMATION:
APPLICANT: Leaby, K.
APPLICANT: MCKAY, C.
APPLICANT: MCKAY, C.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 11
LENGTH: 228
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US-09-336-536-11
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-336-536-4
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US-09-336-536-7
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
Sequence 7, Application US/09336536
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Best Local (
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Best Local Similarity
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                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                  YDAVTGKETCQVPGVYYEAVHATVYRASLQEDLVKNGESIASFEQFEGGWPKPASLSGGA 195
                                                                                                                                                                                                                             PRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGH 135
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illarity 100.0%;
Conservative (
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Pred. No. 2.4e-102;
5; Mismatches 7;
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CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 14
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Best Local :
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APPLICANT: MCKay, C.
APPLICANT: MOSSONE, C.
APPLICANT: BOSSONE, C.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT APPLICATION NUMBER: US/09/336,536
NUMBER OF SEQ LD NOS: 75
NUMBER OF SEQ LD NOS: 75
                                                                                                                                                                                 Matches 121;
                                                                                                                                                                                            Query Match
Best Local Similarity
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APPLICANT: MCKBY, C.
APPLICANT: BOSSONE, S.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
                                                                                                                                                                                                                                                        LENGTH: 128
TYPE: PRT
ORGANISM: Mus musculus
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                          165 QFDLVKNGESIASFFQFFGGWPKPASLSGGAMVRLEPEDQVMVQVGVGDYIGIYASIKTD 224
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128; Conserv
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                            225 STFSGFLV 232
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                                                        QFDLVKNGQSIASFFQYFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTD
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Pred. No. 2.3e-52;
Prematches 3;
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RESULT 9 US-08-463-911-2

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                                                              Sequence 8, Application US/09140804 Patent No. 6197930 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617) 861-9540 NFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 861-6240
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 32,
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                                                                                                                                                                           STETGELLYHD 245
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ilarity 40.6%;
Conservative 3
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Pred. No. 3.4e-32
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US-09-118-408-3
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                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-30
CURRENT APPLICATION NUMBER: US/09/118,408A
CURRENT FILING DATE: 1998-07-17
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SOFTWARE: FastSEQ for Windows Version
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CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapien
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                                                                                                                                  55 RDGAPGAPGEKGEGGRPGLPGPRGDPGPRGEAGPAGP-----TGPAGECSVPPRSA 105
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                                            FSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQ 165
                                                                                        ----GTPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPQTPGRKGEPGEAAYMYRSA
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FSV-GLETRYTVP-NVPIRETKIEYNQQNHYDGSTGKEYCNIPGLYYESYHITVYMKDVK
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                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                         Score 428.5; DB 4; Pred. No. 9.7e-32;
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Pred. No. 9.7e-32;
                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                            Length 247;
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-506-855-3
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CURRENT FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                   Sequence 7, Application Patent No. 5869330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09506855
Patent No. 6448221
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND TITLE OF INVENTION: IMMUNE FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sheppard, Paul O. APPLICANT: Lasser, Gerald W. APPLICANT: Bishop, Paul D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 99-12
                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook,
STREET: Two Militia Drive
                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                               APPLICANT:
                                                                                                                                           NUMBER OF SEQUENCES:
OMPUTER READABLE FORM:
                                   COUNTRY:
                                                                    CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                             235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 FDLVKNGESIASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQV-GVGDYIGIYASIKTD 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101;
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                                                     Massachusetts
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                                     USA
                                                                                                                                                                                             Lodish, Harvey
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A NOVEL SERUM PROTEIN PRODUCED EXCLUSIVELY IN ADIPOCYTES
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Pred. No. 9.7e-32;
                                                                                                      Smith & Reynolds,
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                                                                                           SEQ ID NO 3
LENGTH: 244
TYPE: PRT
ORGANISM: Homo sapiens
Query Match
Best Local Similarity 40.4
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09140804 Patent No. 6197930
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Best Local
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EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/140,804 CURRENT FILING DATE: 1998-08-26
                                                                                                                                                                                                                                                                                APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: WH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 HATVYRASLQFDLVKNGES-IASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQV-GVGD
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                 32.0%;
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Score 424; DB 4; I
Pred. No. 2.5e-31;
Pred. Mismatches 72;
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                                     Length 244;
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   58;
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Gaps
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CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 244
TYPE: PRT
ORGANISM: Homo saplens
US-09-336-536-20
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US-09-336-536-20
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Best Local Similarity
Matches 106; Conserv
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TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       equence 20, Application US/09336536
atent No. 6406884
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221 RNGLYADNDNDSTFTGFLLYHD 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 HITVYMKDVKVSLFKKDKAMLFTYDQYQENNVDQA--SGSVLLHLEVGDQVWLQVYGEGE 220
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                                                                                                                                                 105 GEGAYYYRSAFSV-GLETYVTIP-NMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAY 162
                                     214 YIGIYASIKTDSTFSGFLVYSD 235
                                                                          163 HITVYMKDVKVSLFKKDKAMLFTYDQYQENNVDQA--SGSVLLHLEVGDQVWLQVYGEGE 220
                                                                                                                                                                                                                          51 GAPGRDGRD-----GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP 104
                                                                                                                                                                         96 GECSVPPRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAV 155
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                                                                                                                                                                                                                                                                                                 7 VLLLLAL-----
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                                                                                                                                                                                                                                                                                                                                                                             32.0%; Score 424; DB 4; Length 244; Alarity 40.5%; Pred. No. 2.5e-31; Conservative 26; Mismatches 72; Indels
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Search completed: June 18, 2003, 14:54:23 Job time: 30 secs

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Result
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CA14_MOUSE
C10C_RAT
FA39_HUMAN
CERB_HUMAN
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PSPD_BOVIN
PSPD_HOUSE
PSPD_HAT
PSPD_HUMAN
CA21_RANCA
CA34_HUMAN
CA17_HUMAN
CAC2_HAECO
PSPA_CAVPO
PSPA_CAVPO
PSPA_CAVFA
PSPA_HUMAN
PSPA_BOUSE
PSPA_PIG
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100.0%; Score 243; DB 1; 100.0%; Pred. No. 1.9e-193;

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Pfam; PF01391; C011agen; 2.
PFRNTS; PR00007; COMPLEMNTC1:
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
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                                                                                                                                                                                                  EMBL; AF329839; AAK17963.1; -...
EMBL; BC022187; AAH22187.1; -..
Genew; HGNC:14342; ClQTNF7.
InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2002) to the EMBL/GenBank/DDBJ-I-SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN-I-SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Piddington C.S., Sheppard P.O., Bishop P., Lasser G.W.; "Homo sapiens complement-clq tumor necrosis factor-related Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
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Query Match
Best Local S
Matches 11
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Immunology 78:159-165(1993).

C-1- FUNCTION: CONTRIBUTES TO THE LUNG'S DEFENSE AGAINST INHALED MICROORGANISMS. BINDS STRONGLY MALTOSE RESIDUES AND TO A LESSER EXTENT OTHER ALPHA-GLUCGSYL MOIETIES. IT COULD PARTICIPATE IN THE EXTRACELLULAR REORGANIZATION OR TURNOVER OF PULMONARY SURFACTANT.

C-1- SUBUNIT: OLIGOMERIC COMPLEX OF 4 SET OF HOMOTRIMERS.

C-1- SUBCELLULAR LOCATION: Extracellular.

C-1- SUBCELLULAR LOCATION: Extracellular.

C-1- MISCELLANEOUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND 10% PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS, CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-C).

THYDROPHOBIC PROTEINS (SP-B AND SP-C).

SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pulmonary surfactant-associated protein D precursor (SP-D) (PSP-D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Eukaryota; Metazoa;
                                                                                                                                                                                                                                          InterPro; IPRO00087; Collagen.
InterPro; IPRO01304; Lectin_C.
Pfam; PF00391; Collagen; 2.
Pfam; PF01391; Collagen; 2.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                            EMBL; X75911; CAA53510.1;
PIR; S33603; S33603.
HSSP; P35247; 1808.
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P35246;
                                                                                                                                                                             prOSITE; PS00615; C_TYPE_LECTIN_1; 1.
prOSITE; PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Calcium; Surface film; Gaseous exchange;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EWBL outstation. European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way infield and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 GLPGRDGRDGR
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                                                                                                                                                            Repeat; Coiled coil.
D.
COLLAGEN-LIKE.
COLLED COIL (POTENTIAL).
C-TYPE LECTIN (SHORT FOR
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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Pred. No.
                                                                                                                 BY SIMILARITY.
PULMONARY SURFACTANT-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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n of liver as a site of
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.06;
                          (SHORT FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Best Local S
Matches 11
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01-OCT-1996
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-C57BL/6 X CBA; TISSUE=Lung;

MEDLIXE=9694460; PubMed=7499852;

MOLWAN1 M., White R.A., Guo N., Dowler L.L.

"Mouse surfactant protein-D. cDNA cloning, localization to chromosome 14.";

J. Immunol. 155:5671-5677(1995).
                       This
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Fisher J.H., Sheftelyevich V.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99244602; PubMed-10226065; Lawson P.R., Perkins V.C., Holmskov "Genomic organization of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pulmonary surfactant-associated protein D precursor (SP-D) (PSP-D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
                                                                                                                                                                                                                                                                                                                                                                             "Surfactant protein-D vivo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P50404;
     between
                                                                                                                                                                                                                                                                                                  Strausberg
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SETPD OR SETP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSPD_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                         MILTED (FEB-2001) to the EMBL/GenBank/DDBJ databases.

MICHOORGANISMS. BINDS STRONGLY MALTOSE RESIDUES AND TO A LESSER

MICHOORGANISMS. BINDS STRONGLY MALTOSE RESIDUES AND TO A LESSER

EXTENT OTHER ALPHA-GLUCOSYL MOIETIES. IT COULD PARTICIPATE IN THE

EXTENCELLULAR REORGANIZATION OR TURNOVER OF PULMONARY SURFACTANT.

SUBGUNIT: OLICOMERIC COMPLEX OF 4 SET OF HOMOTRIMERS.

SUBGULILLAR LOCATION: EXLTACELLULAR CONSISTS OF 90% LIPID AND 10%

PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS

CARBOHYDBATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL
                                                   HYDROPHOBIC PROTEINS (SP-B AND SP-C).
SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
   SWISS-PROT entry is copyright. een the Swiss Institute of Bio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
N-LINKED (GLCNAC.
HYDROXYLATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYDROXYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20:953-963(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dowler L.L., Taunes ....

"" cloning, characterization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07D88B24E0AEB2E3
gnt. It is produced through Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
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for lung s
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.073;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          surfactant
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     EMBL outstation
                                                                                                                 COLLAGENOUS

2 SMALL
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                       collaboration
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       PRACE AND CONTRACT OF THE PROPERTY OF THE PROP
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RESULT
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Best Local
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DOMAIN
DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as for modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
"Purification and biochemical characterization collagenous surfactant-associated protein."; Biochemistry 28:6361-6367(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00059; lectin_c; 1. Pfam; PF01391; Collagen; 3. SMART; SM00034; CLECT; 1.
                                                                                                                               Shimizu H., Fisher Voelker D.R.;
                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                             SFTPD OR SFTP4
                                                                                                                                                                                                                                                                             01-FEB-1994
15-JUL-1999
                                                                                                                                                                                                                                                                                                   P35248;
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal; Lectin;
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                                                MEDLINE-90001186;
                                                             TISSUE-Lung
                                                                       SEQUENCE OF
                                                                                                           deduced
                                                                                                                                                                          SEQUENCE FROM N.A.,
                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                           PSPD_RAT
                                                                                                       "Primary structure of rat pulmonary
deduced amino acid sequence.";
                                                                                                                                                    MEDLINE=92112913; PubMed=1370483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF047742; AAD31380.1;
AF047741; AAD31380.1;
AF192134; AAF15277.1;
BC003705; AAF03705.1;
P35247; 1808
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                                                                                                                                                                                                                                                                   surfactant-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         374
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(Rel. 28, Last sequence update)
(Rel. 38, Last annotation updat
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                                                                                              267:1853-1857(1992)
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                                                                        AND 153-180.
                                                                                                                                         J.H.,
                                                                                                                                                                                                            Chordata;
Rodentia;
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COLLED COLL (POTENTIAL).
C-TYPE LECTIN (SHORT FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
LY SIMILARITY.
N-LINKED (GLCANGC. . .) (POT
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Sciurognathi;
                                        Moxley M., Longmore
                                                                                                                                                                                                                                                                    tation update)
protein D precursor (SP-D) (PSP-D)
                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                            Benson
                                                                                                                    surfactant
                                                                                                                                                                                                                                                                                                                            374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SURFACTANT - ASSOCIATED PROTEIN
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thi; Muridae; Murinae; Rat
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[N (SHORT FORM)
                                                                                                                                         В.,
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                              of CP4
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                              (SP-D),
                                                                                                                                            Mason R.J.,
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PSPD_HUMAN
ID PSPD_HUMAN
AC P35247;
DT 01-FEB-1994
DT 01-FEB-1994
DT 16-OCT-2001
DE Pulmonary sp
GN SFTPD OR SF
OS Homo sapien
OC Eukaryota;
OC Mammalia; E
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Best Local
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Pfam; PF00059; lectin_c; 1.

Pfam; PF010391; Collagen; 3.

SMART; SM00034; CLECT; 1.

PROSITE: DEROCCO
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DISULFID
DISULFID
                                 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pulmonary surfactant-associated protein D pre
SFTPD OR SFTP4 OR PSPD.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
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PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Calcium; Surface film;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal; Lectin;
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HSSP; P35247; 1B08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
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SUBCELLULAR LOCATION: EXTRACELLULAR LOCATION: EXTRACELLULAR LOCATION: EXTRACELLULAR CONSISTS OF 90% LIPID AND 10% PROTEIN. THERE ARE 4 SURFACTANT CONSISTS OF 90% LIPID AND 10% CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL HYDROPHOBIC PROTEINS (SP-B AND SP-C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN. SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: CONTRIBUTES MICROORGANISMS. BINDS
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11; Conserv
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     ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Eutheria; Primates; Catarrhini; Hominidae; Homo.
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37561 MW;
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STRONGLY MALTOSE RESIDUES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat; Coiled
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HYDROXYLATION.
HYDROXYLATION.
HYDROXYLATION.
HYDROXYLATION.
N -> E (IN REF.
K -> C (IN REF.
                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                            Score 11;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COILED COIL (POTENTIAL).
C-TYPE LECTIN (SHORT FORM).
BY SIMILARITY.
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N-LINKED (GLCNAC. .
HYDROXYLATION.
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                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                          -> E (IN REF. 2).
-> C (IN REF. 2).
DB2BB5E399DB4A3C CRC64;
                                                                                                                                                                                                                                                                                               Mismatches
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0.074;
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                                                                   (SP-D) (PSP-D)
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three lectin domains of human lung surfactant protein D. Structure 7:255-264(1999).
-I- FUNCTION: CONTRIBUTES TO THE LUNG'S DEFENSE AGAINST MICROORGANISMS. BINDS STRONGLY MALTOSE RESIDUES AND
                     PROSITE; PS00615; C_TYPE_LECTIN_1; 1. PROSITE; PS50041; C_TYPE_LECTIN_2; 1. Glycoprotein; Calcium; Surface film;
                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF TISSUE-Lung, and Amniotic fluid; MEDIINE-92322003; PubMed-1339284; Lu J., Willis A.C., Reid K.B.M.;
                                                                                            Pfam; PF00059; lectin_c; 1.
Pfam; PF01391; Collagen; 4.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99197291; PubMed=10368295; Hakansson K., Lim N.K., Hoppe H.-J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Human surfactant protein D: SP-D contains carbohydrate recognition domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rust K., Grosso L., Z
Cai G.-Z., Crouch E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Lung;
MEDLINE=91378578; PubMed=1898081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       surfactant protein D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Placenta;
                                                                                                                                                                                                                                                   Genew;
                                                                                                                                                                                                                                                                                                   PIR; A45225; A45225.
PIR; S18382; S18382.
                                                                                                                                                                                                                                                                                                                                                        EMBL;
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"Crystal structure of the trimeric alpha-helical coiled-coil and three lectin domains of human lung surfactant protein D.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 60-375 FROM N.A., AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Purification, characterization and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93155122; PubMed-8428971;
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[1]
                                                                                                                                                                         InterPro; IPR000087; InterPro; IPR001304;
                                                                                                                                                                                                                           MIM; 178635;
                                                                                                                                                                                                                                                                              PDB; 1808;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tities requires a license agreement (S send an email to license@isb-sib.ch).
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MISCELLARBOUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND 10% PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS, CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL HYDROENDRYC BOOTENES GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL HYDROENDRYC BOOTENES (SP-D AND SP-C)
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SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                     ; L05485; AAB59450.1;
; L05483; AAB59450.1;
; L05484; AAB59450.1;
; X65018; CAA46152.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. Biophys. 290:116-126(1991).
                                                                                                                                                                                                                                                   HGNC:10803; SFTPD
Lectin;
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Collagen;
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Repeat; Coiled
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Gaseous exchange; Hydroxylation; iled coil; 3D-structure.
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042350;
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                                                                                                                                                                                                       type
Gene
                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Collagen alpha 2(I) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD_RES
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 EMBL; D88764; BAA22380.1; InterPro; IPR000087; Colli InterPro; IPR000885; Fib_4
                                       use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                            Rana catesbelana (Bull frog).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                MEDLINE-97417499; PubMed-9272872;
                                                                                                                                                                                                                                                            TISSUE-Tail;
                                                                                                                                                                                                                          Asahina K., Oofusa K., Obara M., Yosh
"Cloning and characterization of the
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       NCBI_TaxID=8400;
                                                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                     SUBUNIT: TRIMERS OF ONE ALPHA 2(1) AND TWO ALPHA 1(1) CHAINS. TISSUE SPECIFICITY: FORMS THE FIBRILS OF TENDON, LIGAMENTS AND BONES. IN BONES THE FIBRILS ARE MINERALIZED WITH CALCIUM
                                                                                                                                                                                             o I collagen of bullfrog Rana 194:283-289(1997).
                                                                                                                        PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
                                                                                                                                             HYDROXYAPATITE
                                                                                                                                                                                     (FIBRILLAR FORMING
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Anura; Neobatrachia;
 Collagen.
Fib_collagen_C
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M -> T (IN REF. 2).

P -> F (IN REF. 2).

A -> P (IN REF. 2).

T -> A (IN REF. 2).

T -> P (IN REF. 3).

D -> P (IN REF. 3).

E -> EH (IN PPP
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2986B2699FC01A6A
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Q1-CCT-1996 (Rel. 34, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
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probom; pD002078; Fib_collagen_C;
SMART; SM00038; COLFI; 1.
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                                                                    Quinones S., Bernal D., Garcia-Sogo M., Elena S.F., Saus J.; "Exon/Intron structure of the human alpha 3(IV) gene encompassing goodpasture antigen (alpha 3(IV)NC1). Identification of a potentia antigenic region at the triple helix/NC1 domain junction."; J. Biol. Chem. 267:19780-19784(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mariyama M., Leinonen A., Mochizuki T., 1 "Complete primary structure of the human Coexpression of the alpha 3(IV) and alpha
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JOLAA3

Homo sapiens (Human).

Homo sapiens (Human).

Theria; Chordata;

Theria; Primates;
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                                                                                                                                                                                                                                             "Structure of the human type IV collagen
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., VARIANTS AS E-297; R-407; R-640; Q-1215; S-1277; T-1330; E-1334; E-1347 AND C-1661, AN E-162; Y-326; H-408; R-451; L-574; E-1269 AND P-1474. MEDLINE-2104696; PubMed-11134255; MEDLINE-2104696; PubMed-11134255
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                   SEQUENCE OF 1453-1670 FROM N.A. MEDLINE=91353570; PubMed=1882840;
                                                                                                                                                                SEQUENCE OF 1386-1670 FROM N.A., MEDLINE=93015826; PubMed=1400291;
                                                                                                                                                                                                                                           autosomal Alport
                                                                                                                                                                                                                                                        Heidet L., Arrondel C., Forestier L., Cohen-Solal L., Gutlerrez B., Stavrou C., Gubler M.C., Antignac C.; "Structure of the human type IV collagen gene COL4A3
                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
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CARBOXYL-TERMINAL PROPEPTIDE
   Yang-Feng
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N-LINKED (GLCNAC. .) (POTENTIAL)
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     T.L.,
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in alpha 3(IV) collagen ch
ha 4(IV) collagen chains
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       Reeders S.T.;
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VARIANTS R-43;
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-I- SUBCELLULAR LOCATION: CELL SURFACE (POTENTIAL).

-I- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFGRMS; 1 (SHOWN HERE), 2/V AND 3/LS; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER IN THEIR C-TERMINAL NC1 DOMAINS.

-I- TISSUE SPECIFICITY: ALPHA 3 AND ALPHA 4 TYPE IV COLLAGENS ARE COLOCALIZED AND PRESENT ONLY IN BASEMENT MEMBRANES OF KIDNEY, EYE, COCHLEA, LUNG AND BRAIN.

-I- DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE G-Y-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL TRIPLE-HELICAL TO DOMAIN (WHICH MAY CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL TRIPLE-HELICAL TO DOMAIN (WIT (G-Y-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

-I- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPLE REPEATING UNIT (G-Y-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
                                                                                                                                                                                                                                                                                                          Reeders S.T., Smeets H.J.M.;

"Mutations in the type IV collagen alpha 3 (COL4A3) gene in autosomal recessive Alport syndrome.";

Hum. Mol. Genet. 3:1269-1273(1994).

-1- FUNCTION: TYPE IV COLLAGEN IS THE MAJOR STRUCTURAL COMPONENT OF GLOMERULAR BASEMENT MEMBRANES (GBM), FORMING A 'CHICKEN-WIRE' MESHWORK TOGETHER WITH LAWININS, PROTEOGLYCANS AND ENTACTIN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Reng L., Xia Y., Wilson C.B.;
"Alternative splicing of the NC1 domain of the human alpha 3(IV) collagen gene. Differential expression of mRNA transcripts that predict three protein variants with distinct carboxyl regions.";
J. Biol. Chem. 269:2342-2348(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93280184; PubMed=8505332;

Bernal D., Quinones S., Saus J.;
"The human mRNA encoding the Goodpasture antigen is alternatively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Two genes, COL4A3 and COL4A4 coding for the human alpha3(IV) alpha4(IV) collagen chains are arranged head-to-head on chrom
                                                                                                                                                                                                                                   <del>:</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEBS Lett. 424:11-16(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning of the human Goodpasture antigen to be the alpha 3 chain of type IV collagen.";
J. Clin. Invest. 89:592-601(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence and localization of a partial cDNA encoding the human alpha chain of type IV collagen.";
hm. J. Hum. Genet. 49:545-554(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem.
                                                                                                                                                                                                                                            SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS, ALPHA 1(IV) ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE WITH 2 OTHER CHAIMS TO GENERATE TYPE IV COLLAGEN NETWORK.
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N-LINKED GLYCOSYLATION SITE.

PTM: TYPE IV COLLAGENS CONTAIN NUMEROUS CYSTEINE RESIDUES WHICH ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. 12 OF THESE, LOCATED IN THE NCI DOMAIN, ARE CONSERVED IN ALL KNOWN TYPE IV COLLAGENS.
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PTH: Phosphorylated by the Goodpasture antigen-binding protein.
DISEASE: ANTIBODIES AGAINST THE NCI DOWAIN OF ALPHAJ(IV) MEDIATE
THE HUMAN AUTOIMMUNE DISEASE, GOODPASTURE SYNDROME, WHICH IS
CHARACTERIZED BY HEMATURIA AND PULMONARY HEMORRHAGE.
DISEASE: DEFECTS IN COL4A3 ARE ASSOCIATED WITH THE TYPE I
AUTOSOMAL RECESSIVE FORM OF ALPORT SYNDROME, AN HEREDITARY
GLOMERULONEPHROPATHY CHARACTERIZED BY PROGRESSIVE RENAL FAILURE,
HEMATURIA AND DEAFNESS. THE RECESSIVE FORM OCCURS EQUALLY BETWEEN
MALES AND FEMALES.

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x80031; CAA56335.1;
aJ288487; CAC36101.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94327588; PubMed-8051117; Christiano A.M., Greenspan D.S., Lee S., Uitto J.; "Cloning of human type VII collagen. Complete primary sequence of the alpha I(VII) chain and identification of intragenic polymorphisms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                             Gammon W.R., Abernethy M.L., Padilla K.M., Prisayanh P.S., Cook M.E., Wright J., Briggaman R.A., Hunt S.W. III; "Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion proteins in "livelyed in tissue-specific organization of contractions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93338437; PubMed=1307247;
Christiano A.M., Rosenbaum L.M., Chung-Honet L.C.,
Woodley D.T., Pan T.C., Zhang R.Z., Chu M.-L., Bur
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  MEDLINE-92231902; PubMed-1567409;
Tanaka T., Takahashi K., Furukawa F., Im
Molecular cloning and characterization
                                                                     TISSUE-Keratinocytes;
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                                                                                                                                                                 extracellular
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AJ288537; CAC36101.1;
AJ288538; CAC36101.1;
AJ288538; CAC36101.1;
M92993; AAA21610.1;
M92993; AAA19637.1;
M81379; AAA51556.1;
L08650; AAA52044.1;
U02519; AAA18942.1;
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                                                                                              OF 340-675 FROM
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Genomics
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Lin A.N., Dietz H.C., Hovnanian A., Uitto J.,
"A missense mutation in type VII collagen in two
with recessive dystrophic epidermolysis bullosa."
Nat. Genet. 4:62-66(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The carboxyl-terminal half of type VII collagen, inc
collagenous NC-2 domain and intron/exon organization
corresponding region of the COL7Al gene.";
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                                                                                                                                                                                 Christiano A.M., McGrath J.A., Tan K.C., Uitto J.;
"Glycine substitutions in the triple-helical region of type VII collagen result in a spectrum of dystrophic epidermolysis bullosa phenotypes and patterns of inheritance.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Christiano A.M., Lee J.Y.-Y., Chen W.J., Laforgia S., Uitto Pretibial epidermolysis bullosa: genetic linkage to COL7A1 identification of a glycine-to-cysteine substitution in the helical domain of type VII collagen."; Hum. Mol. Genet. 4:1579-1583(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94224777; PubMed=8170945;
Christiano A.M., Ryynaenen M., Uitto J.;
"Dominant dystrophic epidermolysis bullosa: identification of Gly-->Ser substitution in the triple-helical domain of type VI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98041696; PubMed=9375848;
Jaervikallio A., Pulkkinen L., Uitto J.;
"Molecular basis of dystrophic epidermolysis
the type VII collagen gene (COL7A1).";
Hum. Mutat. 10:338-347(1997).
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genotype/phenotype
severity.";
                        Shimizu H., McGrath J.A., Christiano A.M., "Molecular basis of recessive dystrophic egenotype/phenotype correlation in a case of
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MEDLINE-97358588; PubMed-9215684;
Winberg J.-O., Hammami-Hauasii N., Nilssen O.,
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phenotypic severity of recessive dystrophic
J. Invest. Dermatol. 106:766-770(1996).
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"Novel COL7Al mutations in dystrophic
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01-0CT-1996 (Rel. 34, Created)
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16-0CT-2001 (Rel. 40, Last annotation updat
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RESULT 12
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-1- FUNCTION: IN PRESENCE OF CALCIUM IONS, PSAP BING PHOSPHOLIPIDS AND CONTRIBUTES TO LOWER THE SURRE
                                                                                                                                                                                                                                                             DOMAIN
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HSSP; P22897; 1EGG.
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Mammalia; Eutheria; Rodentia;
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SFTPA1 OR SFTPA
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PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Calcium; Surface film; Gaseous
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InterPro; IPR001304; Lectin_C.
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MISCELLANEOUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND MISCELLANEOUS: PULMONARY SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGEN PROTEIN: 1 THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENO GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL HYDROPHOBIC PROTEINS (SP-B AND SP-C).

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIR-LIQUID INTERPACE IN THE ALVEOLI OF THE MAMMALIA ESSENTIAL FOR NORMAL RESPIRATION.
SUBUNIT: OLIGOMERIC COMPLEX OF 6 SET OF HOMOTRIMERS
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N-LINKED (GLCNAC. ..) (POTENTIAL)
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COLLAGEN-LIKE.
C-TYPE LECTIN (SHORT FORM)
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BY SIMILARITY.
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Hystricognathi; Caviidae; Cavia
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SFTPA1 OR
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specific DNase I hypersensitive site.";
Am. J. Physiol. 262:L662-L671(192),
-1- FUNCTION: IN PRESENCE OF CALCIUM IONS, PSAP BINDS TO SURFACTA
PHOSPHOLIPIDS AND CONTRIBUTES TO LOWER THE SURFACE TENSION AT
AIR-LIQUID INTERFACE IN THE ALVEOLI OF THE MAMMALIAN LUNG AND
ESSENTIAL FOR NORMAL RESPIRATION.
-1- SUBBUNIT: OLICOMERIC COMPLEX OF 6 SET OF HOMOTRIMERS.
                                                                  VARIANT
CONFLICT
                                                                                         DOMAIN
DISULFID
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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MEDLINE=92312742; PubMed=
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Pfam; PF01391; Collagen; 2.
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InterPro; IPR001304; Lectin_C.
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SUBCELLULAR LOCATION: EXELTACELLULAR.

MISCELLANEOUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND MISCELLANEOUS: PULMONARY SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGEN CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL HYDROPHOBIC PROTEINS (SP-B AND SP-C).

SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.

SIMILARITY: CONTAINS 1 C_TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute.
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major appprotein of rabhit puln
ary sequence and cyclic AMP and
iol. Chem. 263:2939-2947(1988).
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            Similarity
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PS50041; C_TYPE_LECTIN_2; 1.
tein; Calcium; Surface film; Gaseous
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Boggaram V., Mendelson C
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K., Mendelson C.
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C-TYPE LECTIN (
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              DB 1;
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01-JAN-1988 (Rel. 06, Created)
01-WY-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation A precursor (SP-A) (PSP-A)
       CARBOHYD
                                                                                                                          PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Calcium; Surface film;
                                                                                                                                                                  Interpro; IPRO00087; Collagen.
Interpro; IPRO01304; Lectin_C.
Pfam; PF00059; lectin_C; 1.
Pfam; PF01391; Collagen; 2.
SMART; SM00034; CLECT; 1.
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Canis familiaris (Dog).
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HSSP; P22897; 1EGG.
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Proc. Natl. Acad. Sc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  White R.T.;
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Mammalia; Eutheria; Carnivora;
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                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: IN PRESENCE OF CALCIUM IONS, PSAP BINDS TO SURFACTANT PHOSPHOLIPIDS AND CONTRIBUTES TO LOWER THE SURFACE TENSION AT THE AIR-LIQUID INTERPACE IN THE ALVEOLI OF THE MAMMALIAN LUNG AND IS ESSENTIAL FOR NORMAL RESPIRATION.

SUBGUNIT: OLIGOMERIC COMPLEX OF 6 SET OF HOMOTRIMERS.

SUBCELLULAR LOCATION: EXTRACTIONIAT.

MISCELLANEOUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND 10% PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS, CARBOHYDRAFE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL HYDROPHOBIC PROTEINS (SP-B AND SP-C).

SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.

SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.
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COLLAGEN-LIKE.
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; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82:6379-6383(1985)
                                                                                                                            Gaseous
                                                                                   SURFACTANT-ASSOCIATED PROTEIN
                                           (SHORT
                                                                                                                           exchange; Hydroxylation;
    .) (POTENTIAL).
                                            FORM)
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Canis.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RATUAL S.L., Singh G., Locker J.L.;

RATUAL S.L., Singh G., Locker J.L.;

"Characterization of a second human pulmonary surfactant-associated protein SP-A gene.";

Am. J. Respir. Cell Mol. Biol. 6:446-452(1992).

-i. FUNCTION: IN PRESENCE OF CALCIUM IONS, PSAP BINDS TO SURFACTANT PHOSEHOLIPIDS AND CONTRIBUTES TO LOWER THE SURFACE TENSION AT THE PHOSEHOLIPIDS AND CONTRIBUTES TO LOWER THE SURFACE TENSION AT THE AIR-LIQUID INTERFACE IN THE ALVEOLI OF THE MAMMALIAN LUNG AND IS ESSENTIAL FOR NORMAL RESPIRATION.

-i. SUBGUNIT: OLIGOMERIC COMPLEX OF 6 SET OF HOMOTRIMERS.

-i. SUBGUNIT: OLIGOMERIC COMPLEX OF 6 SET OF HOMOTRIMERS.

-i. SUBCELLULAR LOCATION: EXTRACTANT CONSISTS OF 90% LIPID AND 10% PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS, CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL THE CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL THE PROTECTION (SP-A AND SP-D) AND 3 SMALL THE PROTECTION (SP-A AND SP-D) AND 3 SMALL THE PROTECTION (SP-A AND SP-D) AND 3 SMALL THE PROTECTION (SP-A AND SP-D) AN
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P07714;
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SEQUENCE
                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              White R.T., Damm D., Miller J., Spratt Benson B., Cordell B., "Isolation and characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-86250832; PubMed-3755136; Floros J., Steinbrink R., Jacobs K., Phelps D., Sultzman L., Jones S., Taeusch H.W., Frank H.A., "Isolation and characterization of cDNA clones f pulmonary surfactant-associated protein."; J. Biol. Chem. 261:9029-9033(1986).
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01-APR 1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pulmonary surfactant-associated protein A precursor (SP-A) (PSP-A)
(PSAP) (Alveolar proteinosis protein) (35 kDa pulmonary surfactant-
   EMBL; M13686; EMBL; K03475;
                                                                                                                                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       apoprotein gene.";
Nature 317:361-363(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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SFTPA1 OR SFTPA OR SFTP1 OR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN. SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYDROPHOBIC PROTEINS (SP-B AND SP-C)
                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 GLPGRDGRDG
|||||||||
40 GLPGRDGRDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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AAA36520.1;
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26268 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49
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Pred. No.
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H.A., Fritsch E.F.;
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RESULT 15
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ID PSPA_M
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DISULFID
CARBOHYD
        Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                              01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pulmonary surfactant-associated protein A pre
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PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

Glycoprotein; Calcium; Surface film; Gaseous exchange; Hydroxylation;
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Pfam; PF01391; Collagen; 2.
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Genew; HGNC:10798; SFTPA1.
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InterPro; IPR001304; Lectin_C.
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REF. 2; AAA36510).
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Search completed: June 18, Job time: 32 secs

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Pfam; PF01391; Collagen; 2.
SMART; SM00034; CLECT; 1.
PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Calcium; Surface film; Gaseous
                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transcriptional activity.";
Am. J. Physiol. 263:1546-1554(1992).
-i- FUNCTION: IN PRESENCE OF CALCIUM
PHOSPHOLIPIDS AND CONTRIBUTES TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Korfhagen T.R., Bruno M.D., Glasser S.W., Ciraolo P.J., Whitsett Lattier D.L., Wikenheiser K.A., Clark J.C.;
"Murine pulmonary surfactant SP-A gene: cloning, sequence, and
                                                                                                                                                                                                                                      Signal; Lectin;
SIGNAL 1
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SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Extracellular.

MISCELLANEOUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGEN CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL HYDROPHOBIC PROTEINS (SP-B AND SP-C).

SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: IN PRESENCE OF CALCIUM IONS, PSAP BINDS TO PHOSPHOLIPIDS AND CONTRIBUTES TO LOWER THE SURFACE I PHOSPHOLIPIDS AND CONTRIBUTES TO LOWER THE SURFACE IN THE ALVOLI OF THE MAMMALIAN AIR-LIQUID INTERFACE IN THE ALVOLI OF THE MAMMALIAN ESSENTIAL FOR NORMAL RESPIRATION.

SUBUNIT: OLIGOMERIC COMPLEX OF 6 SET OF HOMOTRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                      A48853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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C-TYPE LECTIN (SHORT FORM).
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (PROBABLE).
M-6688BF070E3EB9AE CRC64;
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PULMONARY SURFACTANT-ASSOCIATED PROTEIN
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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## ALIGNMENTS

gelatin-binding 28K protein precursor - human

N;Alternate names; adipose specific collagen-like factor

C;Species: Homo sapiens (man)

C;Date: 10-May-1996 #sequence\_revision 19-Jul-1996 #text\_change 20-Sep-1999

C;Accession: JC4708; JC4944

R;Maeda, K.; Okubo, K.; Shimomura, I.; Funahashi, T.; Matsuzawa, Y.; Matsubara, K.

Blochem. Blophys. Res. Commun. 221, 286-289, 1996

A;Title: cDNA cloning and expression of a novel adipose specific collagen-like factor
A;Reference number: JC4708; MUID:96224171; PMID:8619847

A;Accession: JC4708 C;Accession: T14782 R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, August 1999 hypothetical protein DKFZp586B0621.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 02-Sep-2000
C;Accession: T14782 A;Note: DKFZp586B0621.1
C;Superfamily: complement Clq carboxyl-terminal homology A; Molecule type: mRNA A; Residues: 1-219 <OTT> A; Reference number: Z18184 A; Accession: T14782 A; Experimental source: adult uterus; clone DKFZp586B0621 A; Cross-references: EMBL: AL110261 A;Status: preliminary Matches Query Match Match 91.1%; Score 1207; I Local Similarity 100.0%; Pred. No. 1.: les 219; Conservative 0; Mismatches 181 205 121 145 61 85 25  $\vdash$ Score 1207; DB 2; Length 219; Pred. No. 1.3e-77; O; Mismatches 0; Indels 0 Gaps 180 144 60 204 120 0

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A; Molecule type: mRNA
A; Residues: 1-244 < KARE>
A; Cross references: DDBJ:D45371; NID:9871886; PIDN:BAA08227.1; PID:9871887
A; Cross references: DDBJ:D45371; NID:9871886; PIDN:BAA08227.1; PID:9871887
A; Experimental source: adipose tissue
R; Makano, Y; Tobe, T; Choi-Miura, N.H.; Mazda, T; Tomita, M.
J. Biochem. 120, 803-812, 1996
A; Title: Isolation and characterization of GBP28, a novel gelatin-binding protein purif
A; Title: Isolation and characterization of GBP28, a novel gelatin-binding protein purif
A; Terence number: JC4944
A; Molecule type: protein
C; Comment: This protein is an endogenous factor that binds with a collagen-like domain.
C; Genetics:
A; Gene: apM1
C; Superfamily: unassigned collagens; complement C1q carboxyl-terminal homology
C; Moywords: adipose tissue; glycoprotein; hydroxyproline
F; 1-18, Domain: signal sequence # Status prodicted < SIG>
C; Comment: This protein is an endogenous factor that binds with a collagen-like domain.
C; Superfamily: unassigned collagens; complement C1q carboxyl-terminal homology
C; Moywords: adipose tissue; glycoprotein; hydroxyproline
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                                                                                                                                                                                                    A; Reference number: S30085
A; Accession: S30086
A; Moleonia
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A;Cross-references: EMBL:X65120; NID:g23129
A;Note: the initial difference is probably due
R;Apte, S.; Mattel, M.G.; Olsen, B.R.
FEBS Lett. 282, 393-396, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-680 < REI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collagen alpha 1(X) chain precursor - human
N;Alternate names: procollagen alpha 1(X) chain
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                                                                                                                                                   A; Molecule type: DNA
A; Residues: 'TIPFYGWVCWVCLL', 52-680 <APT>
                                                                                                                                                                                                                                                                                                                                                            R;Apte, S.S.
                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X68952; EMBL:X72578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142-107/Region: collagen-like complement Clq carboxyl-terminal homology <ClQ>
95/Modified site: 4-hydroxyproline (Pro) #status experimental complemental carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: unassigned collagens; complement Clq carboxyl-terminal homology; superfamily: unassigned collagens; complement Clq carboxyl-terminal homology; Roywords: adipose tissue; glycoprotein; hydroxyproline; ladipose tissue; glycoprotein; hydroxyproline; ladipose tissue; glycoprotein; hydroxyproline; ladipose tissue; ladipo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 RNGLYADNDNDSTFTGFLLYHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 GECSVPPRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 GAPGRDGRD-----GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
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Pred. No. 7
                                                                                                                                                                                                                                                                                                                       March
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                                                                                 to translation of an intronic
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A; Introns: 52/1
            В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: GDB: COL10A1
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            521
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A; Molecule type: DNA
A; Residues: 561-647, 'G', 649-666 < AP2>
A; Residues: 561-647, 'G', 649-666 < AP2>
A; Cross-references: EMBL: X58879; NID: 930013; PIDN: CAA41686.1; PIR: Thomas, J.T.; Cresswell, C.J.; Rash, B.; Nicolai, H.; Jones, T.
Blochem, J. 280, 617-623, 1991
A; Title: The human collagen X gene. Complete primary translated A; Reference number: S18249; MUID: 92109659; PMID: 1764025
A; Accession: S18249
A; Molecule type: DNA
A; Residues: 1-26, 'T', 28-680 < THO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homolog C;Keywords; coiled coil; extracellular matrix; 9lycoprotein; homotrimer; hydroxylysin F;1-18/Domain: signal sequence #status predicted <SIG> F;19-680/Product: collagen alpha 1(X) chain #status predicted <MAT> F;19-56/Domain: amino-terminal nonhelical #status predicted <NC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Note: a defect in this gene may C; Complex: type X collagen may be C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: mutant sequence from patient with metaphyseal chondrodysplasia type A;Note: a second mutant sequence with 614-Pro is also described C;Comment: Prolines and lysines at the third position of the tripeptide repe ed and subsequently O-glycosylated.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;57-519/Region: interrupted helical #status predicted <NCl>
F;520-680/Domain: amino-terminal nonhelical #status predicted <NCl>
F;553-679/Domain: complement Clq carboxyl-terminal homology <ClQ>
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A;Molecule type: mRNA
A;Residues: 520-597,'D',599-680 <WAL>
A;Cross-references: GB:S68531; NID:g545180; PIDN:AAC60615.1; PID:g545181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;553-679/Domain: complement Ciq
F;617/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Description: structural component of extracellular fibrous polymer specifically and be important for skeletogenesis
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                                                                                                                                                                                                                                                                                                                                                                                                          401 GNPGLPGPKGDPGVGGPPGLPGPVGPAGAKGMPGHNGEAGPRGAPGIPGTRGPIGPPGIP
                                                                                                                                                                                                                                                                      461 GFPGSKGDPGSPGPPGPAGIATKGLNGPTGPPGPPGPRGHSGEPGLPGPPGPPGPPGQAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 GSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLP
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                                                                                                                                   MPEGFIKAGQRPSLSGTPLVSANQGVTGMPVSAFTVILSKAY--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.6%; Score 418.5; DB 1; 34.9%; Pred. No. 5.4e-22; ative 34; Mismatches 82;
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engrada e.
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A;Accession: A;Accession: A;Accession: A;Accession: A;Molecule type: mRNA
A;Residues: 1-75 < CLUY
A;Residues: 1-75 < CLUY
R;Ninomiya, Y:; Gordon, M.; van der Rest, M.; Schmid, T.; Lir
Biol. Chem. 261, 5041-5050, 1986
A;Title: The developmentally regulated type X collagen gene
A;Reference number: I50218; MUID:86168227; PMID:3082876
A;Accession: S65594
A;Accession: S65594
A;Accession: DNA
A;Accession: DNA
A;Accession: DNA
A;Accession: DNA
A;Accession: S65594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;LuValle, P.; Ninomiya, Y.; Rosenblum, N.D.; Olsen, B.R. J. Biol. Chem. 263, 18378-18385, 1988
A;Title: The type X collagen gene. Intron sequences split the A;Reference number: A31896; MUID:89054019; PMID:2461368
A;Accession: A31896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            collagen alpha 1(X) chain precursor - chicken
N;Alternate names: type X collagen
C;Species: Gallus gallus (chicken)
C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999
C;Accession: S2329; A31896; S65594; S77711; T50218
R;Ninomiya, Y; Castagnola, P; Gerecke, D.; Gordon, M.K.; Jacenko, O.; Luve maguchi, N; Olsen, B.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 104-112, 'X', 114-117; 453-466 <NIN2>
C; Superfamily: collagen alpha 1(VIII) chain; complement C1q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Mostdues: 'T', 9, 'D', 11-12, 'EDOMKLYILFTM', 30-31, 'TCKSGRAFTTYMILONVMADLVSSHT', 48-89, 'L'
629', 'PQAVLSLISMRTIKCGSSCOTONPMYSIPLMMFILLSQVSYLLKSNNIPLTMS' <NIN1>
A; Cross-references: EMBL:M13496; NID:g211699; PIDN:AAA48736.1; PID:g211700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-674 <NIN>
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F;547-673/Domain: complement Clq carboxyl-terminal homology <ClQ>
F;453,456/Modified site: hydroxyproline (Pro) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: S23297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;611/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reywords: coiled coil; extracellular matrix; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                     468
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RIPGLYYFSYHVHAKGTNVWVALYKNGSPVMYTYDEYQKGYLDQA--SGSAVIDLMENDQ
                                                                                                  GMSFMKAGANQALTGMPVSAFTVILSKAY--PGATVPIKFDKILYNRQQHYDPRTGIFTC
                                                                                                                                                                                                                                                       PGPR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGSAIIDLTENDQVWLQLPNAESNGLYSSEYVHSSFSGFLV 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGGAMVRLEPEDOVWVQVGVGDYIGIYASIKTDSTFSGFLV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIA-SFFQFFGGWPKPASL 191
                                                 QVPGVYYFAVHATVYRASLQFDLVKNGESIA-SFFQFFGGWPKPASLSGGAMVRLEPEDQ
                                                                                                                                                                                                     PGPAGIATKGLRGPMGPPGPPGPKGNSGEPGLPGPPGPPGPPGQSTIPEGYVKGESRELS
                                                                                                                                                                                                                                                                                                      AGPPGLPGPVGPQGVKGVPGINGEPGPRGPSGIPGIRGPIGPPGMPGAPGAKGEAGAPGL
                                                                                                                                                                                                                                                                                                                                                                                                                           31.4%;
                                                                                                                                               PRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTC
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                                                                                                                                                                                                                                                                                                                                                                                                      34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 416.5;
                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 7.3e-22;
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; homotrimer; hydroxyproline
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A;Gene: CCL10A1
A;Gene: CCL10A1
C;Superfamily: collagen alpha l(VIII) chain; complement Clq ca
C;Superfamily: collagen alpha l(VIII) chain; glycoprotein; h
C;Keywords: collagen alpha l(X) chain #status predicted
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-674/Product: collagen alpha l(X) chain #status predicted
F;19-674/Product: complement Clq carboxyl-terminal homology <C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X66295; NID:g50228; PIDN:CAA46993.1; PID:g50229 C;Superfamily: complement subcomponent Clq chain A; complement Clq carbo: F;122-245/Domain: complement Clq carboxyl-terminal homology <ClQ>
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                                                                                                                                                                                                                                                           R:Thomas, J.T.; Kwan, A.P.L.; Grant, M.E.; Boot-Handford, R.P. Blochem. J. 273, 141-148, 1991
A:Title: Isolation of cDNAs encoding the complete sequence of bovine type X collagen. A;Reference number: S13301; MUID:91113131; PMID:1703407
A;Accession: S13301
                                                                                                                                                                                                                                                                                                                                                          collagen alpha 1(X) chain precursor - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 21-Nov-1993 #sequence_revision 23-Feb C;Accession: S13301
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A; Residues: 1-246 <PET>
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A; Residues: 1-674 <THO>
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103;
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                                                                                                                                                                                                   EMBL: X53556; NID: g263; PIDN: CAA37624.1; PID: g264
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31..18;
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Score 411.5;
Pred. No. 1.6
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Pred. No. 5.4e-22;
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                    DB 2;
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                    Length
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Similarity

Conservative

Mismatches

Indels

61;

Gaps

6,

1.6e-21

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collagen alpha 1(X) chain precursor - mouse
C.Species: Mus musculus (house mouse)
C.Species: Musculus (house mouse)
R.Kong, R.Y.C.; Kwan, K.M.; Lau, E.T.; Thomas, J.T.; Boot-Handford, R.P.; Grant, M.E.;
Bur. J. Blochen. 211, 99-111, 1993
A.Title: Intron-exon structure, alternative use of promoter and expression of the mouse
A.Refarence number: S1216; MUID:9238750; PMID:847738
A.Accession: S1216
A.Accession: S1216
A.ACCESSION: S28807; MUID:9238750; PMID:8424763
A.TILLE: The mouse collagen x gene: complete nucleotide sequence, exon structure and e
A.Refarence number: S28807; MUID:93143576; PMID:8424763
A.ACCESSION: S28807; MUID:93143576; PMID:8424763
A.ACCESSION: S28807; MUID:93143576; PMID:8424763
A.ACCESSION: S28807; MUID:93143576; PMID:944763.1; PID:950481
R.Elima, K.; Metasarnta, M.; Kallio, J.; Peraelae, M.; Berola, I.; Garofalo, S.; de C
Blochim. Biophys: Acta 1130, 78-80, 1992
A.TILLE: The mouse collagen x gene: complete nucleotide sequence, exon structure and e
A.Reference number: S2215; MUID:92182017; PMID:944763.1; PID:950481
A.Residues: 1.285, A., 287-680 (stil)
A.ACCESSION: S28807; MUID:92182017; PMID:944763.1; PID:950481
A.Residues: 1.285, A., 287-680 (stil)
A.ACCESSION: S22215; MUID:92182017; PMID:1543751
A.ACCESSION: S22215; MUID:92282017; PMID:1543751
A.ACCESSION: S22215; MUID:92282
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                ;Molecule type: DNA
;Residues: 52-247, 'L', 249-285,'A', 287-305,'F', 307-416,'S', 418-499, 'L', 501-566,'C'
;Residues: 52-247, 'L', 249-285,'A', 287-305,'F', 307-416,'S', 418-499, 'L', 501-566,'C'
;Cross-references: EM5L:X65121; NID:950482; PION:CAA46237.1; PID:9667031
;Cross-references: EM5L:X65121; NID:950482; PION:CAA46237.1; PID:9667031
;Summers, T.A.; Irwin, M.H.; Mayne, R.; Ballan, G.
;Summers, T.A.; Irwin, M.H.; Mayne, R.; Ballan, G.
;Summers, T.A.; Irwin, M.H.; Mayne, R.; Ballan, G.
;Blol. Chem. 263, 581-587, 1988
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C;Genetics:
A;Gene: GDB:ClQG
A;Gene: GDB:ClQG
A;Gene: GDB:ClQG
A;Gross-references: GDB:128132; OMIM:120575
A;Map position: 1p36.3-1p34.1
A;Introns: 60/3
A;Introns: 60/3
C;Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal C;Superfamily: complement pathway; glycoprotein; homodimer; hydroxylysine; hydroxyprolin F;1-28/Domain: signal sequence #status predicted <SIG>
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A; Reference number: $26397; MUID:88087150; PMID:2826450
A; Accession: $26397
A; Molecule type: protein
A; Residues: $SOXTESQ', 24-26,'KQ' <SUM>
C; Genetics:
A; Gene: Colloa-1
A; Map position: 10
A; Introns: 51/3
C; Superfamily: collagen alpha 1(VIII) chain; complement Ciq carboxyl-te
C; Keywords: Colled coil; extracellular matrix; glycoprotein; homotrimer
F; 1-18; Domain: signal sequence #status predicted <SUC>
F; 19-680/Product: collagen alpha 1(X) chain #status predicted <MAT>
F; 553-679; Domain: complement Ciq carboxyl-terminal homology <CiQ>
Blochem, J. 179, 367-371, 1979

Britle: Complete amino acid sequences of the three collagen-like regions present 1

A; Fitle: Complete amino acid sequences of the three collagen-like regions present 1

A; Reference number: A90304; MUID:80020137; PMID:486087

A; Rocession: A03207

A; Molecule type: protein

A; Residues: 29-56, 'p',58-65, 'K',67-71, 'p',73-83, 'K',85-86,'D',88-89,'N',91-122 <REI

C; Comment: The first component of complement is a calcium-dependent complex of the ivation of Clr (enzyme), Cls (proenzyme), and the other eight components of complem C; Comment: The Clq subcomponent is composed of nine subunits, six of which are disurbiners of the C chain. Equimolar amounts of the A, B, and C chains are found after
                                                                                                                                                                                                                                                                                                                                                                                                                       complement subcomponent Clq chain C precursor - N;Alternate names: complement subcomponent Clq C;Species: Homo sapiens (man) C;Date: 22-May-1981 #sequence_revision 31-May-1 C;Accession: $14351; A03207 R;Sellar, G.C.; Blake, D.J.; Reid, K.B.M. Blochem, J. 274, 481-490, 1991
                                                                                                                                                                                                                                                                            A;Title: Characterization and organization A;Reference number: $14350; MUID:91174759; A;Accession: $14351
A;Status: not compared with conceptual trana,Molecule type: DNA
A;Residues: 1-245 <SEL>
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C1HUQC
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R; Reid, K.B.M.
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J. Biol. Chem. 264, 16022-16029, 1989
A; Title: The cloning and sequencing of alphal(VIII) collagen omains similar to those of type X collagen.
A; Reference number: A34246; MUID:89380199; PMID:2476437
A; Accession: A34246
                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:J05042; NID:g164895; PIDN:AAA31204.1; PID:g164896 C;Superfamily: collagen alpha 1(VIII) chain; complement Ciq carboxyl-term F;1-20/Domain: signal sequence #status predicted <STG> F;21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT> F;21-117/Region: amino-terminal nonhelical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;29-245/Product: complement subcomponent C1q chain B #status predicted F;31-114/Domain: collagenous, triple helix <COL>
F;31-121-244/Domain: complement C1q carboxy1-terminal homology <C10>
F;121-244/Domain: complement C1q carboxy1-terminal homology <C10>
F;32/D1sulfide bonds: interchain #status experimental
F;36,39,42,45,54,63,81,93,96,99,105/Modified site: 4-hydroxyproline (Pro)
F;57,72,72,75/Modified site: 5-hydroxylysine (Lys) #status experimental
F;75/Binding site: carbohydrate (Lys) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-744 < YAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: A34246
R; Yamaguchi, N.; Ber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       collagen alpha 1(VIII) chain precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
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145
                                  595 VKTPHAYAAKKGKNGGPAYEMPAFTAELTAPFPPVGAPIKFDRLLYNGRONYNPQTGIFT
                                                                                                        535 PGVAGLHGPPGKPGALGPQGQPGLPGPPGPPGPPGPPAVMPPTPAPQGEYLPDMGLGIDG
                                                                                                                                                                               475 VPGLLGPKGEPGIPGDQGLQGPPGIPGITGPSGPIGPPGIPGPKGEPGLPGPPGFPGVGK 534
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                                                                                                                                           -----GPRGDP---GPRGE---AGPAGPTGPAGECSVPPRS-----
CQVPGVYYFAVHATVYRASLQFDLVKNGESIA-SFFQFFGGWPKPASLSGGAMVRLEPED
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Pred. No. 4.3e-21;
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Pred. No. 7
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C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision
C:Accession: $23298
P.Ninner:
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S23779
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A; Accession: S23298
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                  R;Muragaki, Y.; Shiota, C.; Inoue, M.; Ooshima, A.; Olsen, Bur. J. Biochem. 207, 895-902, 1992
A;Title: Alpha-1(VIII)-collagen gene transcripts encode a A;Reference number: S23779; MUID:92362626; PMID:1499564
A;Accession: S23779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collagen alpha 1(VIII) chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: $23779
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                                                                                                                                                    A;Cross-references: EMBL:x66976; NID:g50493; PIDN:CAA47387.1; PID:g1359953 C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-termif;616-742/Domain: complement Clq carboxyl-terminal homology <ClQ>
                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-743 <MUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GPRGDP---GPRGE---AGPAGPTGPAGECSVPPRS-----
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                                         27.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sandell L.J. and Boyd C.D., eds., pp.79-114, Avoid collagens with short triple-helical domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 370; DB 1;
Pred. No. 1.4e-18;
                                         Score 363.5;
Pred. No. 4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-Sep-1999 #text_change 10-Sep-1999
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                                             4.1e-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -PPSDAPLPFDRVLVNEQGHYDAVTGKFT
                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.; Olsen, B.R.; Ninomiya, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 744;
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                                                                              Length 743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 short-chain
                                                                                                                                                                                                     carboxyl-terminal homolog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Conservative

35;

Mismatches

Indels

71;

Gaps

7;

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R; Muragaki, Y.; Jacenko, O.; Apte, S.; Mattei, M.G.; Ninomiya, Y.; Olsen, B.R. J. Biol. Chem. 266, 7721-7727, 1991
A;Title: The alpha2(VIII) collagen gene. A novel member of the short chain collagen A; Reference number: A57131; MUID:91210292; PMID:2019595
A;Accession: A57131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       collagen alpha 2(VIII) chain - human (fc; Species: Homo sapiens (man) C: Date: 03-Nov-1995 #sequence_revision C: Accession: A57131 R; Muraqaki, Y:; Jacenso, O.; Apte, S:;
RESULT
C1HUQB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology F;1-11/Domain: amino-terminal nonhelical (fragment) #status predicted <NC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-635 <MUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: GDB:COL8A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                    13
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                                                                                                                                                                                                                                                                                                                   456
                                                                                                                                                                                                                                                                                                                                                                                              401 GLQGPAGPIGPQGLPGL-KGEPGLPGPPG----EGRAGEPGTAGPRGPPGVPGSPGITGP
                                                                                                                 232 V 232
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                                                                                                                                                                                                                                                                                                                                          71 PGLPGPRGDPGPRGEAGPAG----PTGPA---------GECSVPPRSAFSAKRSE
                                                                                                                                                                                                                                                                                                                                                                                                                                     11 GLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIA-SFFQFFGGWPKPASLSGGAMVRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIDGVKTPHAYAGKKGKHGGPAYEMPAFTAELTVPFPPVGAPVKFDKLLYNGRQNYNPQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLPGPRGDP-----
                                                                                                                                                          VPATYTYDEYKKGYLDQA--SGGAVLQLRPNDQVWVQIPSDQANGLYSTEYIHSSFSGFL
                                                                                                                                                                                                                                                          SRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPGDQVFLQNPFEQAAGLYAGQYVHSSFSGYLLY 741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIFTCEVPGVYYFAYHVHCKGGNVWVALFKNNEPMMYTYDEYKKGFLDQA--SGSAVLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIVGPSGPIGPPGIPGPKGEPGLPGPPGF
                                                                                                                                                                                                                                     PL--PASGMPVKFDRTLYNGHSGYNPATGIFTCPVGGVYYFAYHVHVKGTNVWVALYKNN
                                                                                                                                                                                                                                                                                                                 PGLPGPPGAPGAFDETGIAGLHLPNGGVEGAVLGKGGKPQFGLGELSAHATPAFTAVLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGVGKPGVAGLHGPPGKPGALGPQGQPGLPGPPGPPGPPGPPAVMPTPSPQGEYLPDMGL
                                                                                                                                                                                              -ESIASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2(VIII) chain - human (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.4%; Score 363; 38.6%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GPRGE---AGPAGPTGPAGECSVPPR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SESRVP-PPSDAPLPFDRVLVNEQGHYDAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIDN: AAA62822.1; PID: g177179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .8e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 28-253 <RE1>
A; Cross-references: EMBL: X03084
A; Note: the authors translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: B23422
A; Molecule type: DNA
A; Residues: 'HS', 1-32 <REI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. J. 179, 367-371, A; Title: Complete amino ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: the authors translated A; Accession: A23422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Reid, K.B.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Reid, K.B.M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: GDB:C1QB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. 231, 729-735, 1985
                                                                              64
                                                                                                                     13
                                                                                                                                            4 LLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGRDGAPGAPG
                                                                                                                                                                                                Similarity 36.9
90; Conservative
                                                                            EKGEGGRPGLPGPRGDPGPRGEAGP-----AGPTGPAGECSVPPRSAFSAKRSESR 114
                                                                                                                   LMLLLLLGLIDISQAQLSCTGPPAIPGIPGIPGTPGPDGQPGTPGIKGEKGLPGLAGDHG
  VPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGE-
                                         IPGNPGKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAFSATRT-IN
                                                                                                                                                                                                                    27.38;
36.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                  36;
                                                                                                                                                                                                                    Score 362; DB 1;
Pred. No. 1.7e-18;
                                                                                                                                                                                                  Mismatches
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3

100;

18;

Gaps

72 63

173

Length 253; Indels

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A; Molecule type: protein
A; Residues: 'E', 29-84, 'D', 86-99, 'p', 101-135 <RE5>
A; Residues: 'E', 29-84, 'D', 86-99, 'p', 101-135 <RE5>
R; Reid, K.B.M.; Thompson, E.O.P.
Blochem. J. 173, 863-868, 1978
A; Reference number: A90301; MUID:79041552; PMID:708376
A; Accession: A90301
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 28-99, 'p', 101-195 <RE3>
A; Residues: 13-59, 569, 1982
A; Residues: 13-59, 1982
A; Residues: 13-59, 1982
A; Ritle: Completion of the amino acid sequences of the A and B chains of subcomponent A; Residues: 136-253 <RE4>
A; Molecule type: protein
A; Recidues: 136-253 <RE4>
A; Note: 176-Glx may also be present
C; Comment: The first component of complement is a calcium-dependent complex of the th
Ivation of Clr (enzyme), Cls (proenzyme), and the other eight components of complement
C; Comment: The Clq subcomponent is composed of nine subunits, six of which are disulf
(see PIR:C1HUQC) chain. Equimolar amounts of the A, B, and C chains are found after r
A;Map position: 1p36.3-1p34.1
C;Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal C;Superfamily: complement subcomponent Clq chain B; hydroxylysine; hydroxyprol F;12-27/Domain: signal sequence #status predicted <SIG>F;12-27/Domain: signal sequence #status predicted <SIG>F;28-253/Product: complement subcomponent Clq chain B #status experimental <MAT>F;33-116/Domain: collagenous, triple helix <COL>F;123-249/Domain: complement Clq carboxyl-terminal homology <CIO>F;123-249/Domain: complement Clq carboxyl-terminal homology <CIO>F;123-249/Domain: complement clq carboxyl-terminal homology <CIO>F;123-249/Domain: complement clq carboxyl-terminal homology <CIO>F;135-38/Modified site: pyrrolidone carboxyl-terminal homology *CIO>F;35/Modified bonds: interchain (to chain A-26) #status experimental F;35,38,41,53,56,65,83,86,101,104,107/Modified site: 4-hydroxyproline (Pro) #status experimental F;59,62,77,92,98,110/Modified site: Carbohydrate (Lys) (covalent) #status experimental F;59,62,98,110/Modified site: carbohydrate (Lys) (covalent) #status experimental
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A;Title: Molecular cloning and characterization of the complementary
A;Reference number: A23422; MUID:86076906; PMID:3000358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 22-May-1981 #sequence_revision 31-May-1996 #text_change 08-Dec-2000
C;Accession: B23422; A23422; B90304; A90301; B90315; A03206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement subcomponent C1q chain B precursor [validated] - N; Alternate names: complement subcomponent C1q beta chain
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A;Description: cDNA cloning and expression of the mRNA encoding the B-chain of A;Reference number: S49158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement protein Clq beta chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 20-Aug-1999
C;Accession: S49158
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                                                                          A; Molecule type: mRNA
A; Residues: 1-744 < MUR>
                                                        A; Cross-references:
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                                                                                                            A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: EMBL:X71127; NID:g510191; PIDN:CAA50440.1; PID:g510192; Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal hon; 121-249/Domain: complement Clq carboxyl-terminal homology <
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;Residues: 1-253 <SCH>
Cross-references: GDB:128104; OMIM:120251
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Best Local
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                    GDB:COL8A1
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                                                                                                                                                                                                                                                                                                                                                                                                                          213 DYIGIYASIKTDSTFSGFLVYSD 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 VYSD 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRPLLVLLLLGLAAGSPPLDDNKIPSLC---PGHPGLPGTPGHHGSQGLPGRDGRDGRDG
                                                                                                                                                                                                                                                                                                                                                                                        SLLGVEGA---NSIFTGFLLFPD 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FDLVKNG-----ESIASF------FQFFGGWPKPASLSGGAMVRLEPEDQVWVQ-VGVG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APGAP-----GEKGEGGRPGLP---GPRGDPGPRGEAGPAGPTGP---AGECSVPPRSA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LFPD 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNIVRGRDRDRMQKVLTFCDYAQNTFQV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQ 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPGLAGDHGELGEKGDAGIPGIPGKVGPKGPVGPKGAPGPPGPRGPKGGSGDYKATQKVA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTPLL-LLLLGL-----LHVSWAQSSCTGSPGIPGVPGIPGVPGSDGKPGTPGIKGEKG
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                                                    EMBL: X57527; NID: g30081; PIDN: CAA40748.1; PID: g30082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGGVVLKLEQEEVVHLQATDKN 230
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A;Map position: 3q11.1-3q13.2 (;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homolog F;1-20/Domain: signal sequence #status predicted <SIG>F;21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>F;21-117/Region: amino-terminal nonhelical
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Best Local
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                                      204
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                                                                                                                                                                                                                                                                                                                                                              24 IPSLC--PGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLP-----
                                                                                                                                                                                                                                                                                                                                                                                                           ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
RVFLQMPSEQAAGLYAGQYVHSSFSGYLLY
                                   QVWVQVGVGDYIGIYASIKTDSTFSGFLVY
                                                                            CEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYDEYKKGFLDQA--SGSAVLLLRPGD 712
                                                                                                                    CQVPGVYYEAVHATVYRASLQEDLVKNGESIA-SFFQFFGGWPKPASLSGGAMVRLEPED 203
                                                                                                                                                            VKPPHATGAKKGKNGGPAYEMPAFTAELTAPFPPVGGPVKFNKLLYNGRQNYNPQTGIFT
                                                                                                                                                                                                    VPPRSAFSAKRSESRVP-------PPSDAPLPFDRVLVNEQGHYDAVTGKFT 144
                                                                                                                                                                                                                                          PGVAGLHGPPGKPGALGPQGQPGLPGPPGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDG 594
                                                                                                                                                                                                                                                                                    -----GPRGDPGPRGEAGPAGPTGP----
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          27.1%;
                                                                                                                                                                                                                                                                                                                                                                                                           33;
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 359; DB 2;
Pred. No. 8.5e-18
                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                      233
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 744;
                                                                                                                                                                                                                                                                              -----AGECS 99
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                                                                                                                                                                                                                                                                                                                                                                                                           62;
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Search completed: June 18, 2003, 14:53:59 Job time: 53 secs

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Minimum DB
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No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq length: 0 seq length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
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1325
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                                                                                                 100.0
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:
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/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
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AAB33461
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AAY17827
                                                                                                                             AAY71468
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Human tumour assoc
Human PRO344 prote
Human adipocyte-sp
Human PRO344 prote
Human PRO344 prote
Amino acid sequenc
Human PRO344 polyp
Human PRO344 polyp
Human TANGO 253 SE
Human adipocyte co
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32.0	32.0	•	•	•	•	•	•	32.0	32.1	32.7	32.7	32.7	٠	33.9	36.1	•	50.9	٠	•		•	٠	•	94.8	٠	•	٠	95.9		٠	99.7	•	•	100.0
244	244	244	244	244	244	244	247	247	244	247	247	247	333	225	151	128	128	201	220	228	242	243	243	243	228	243	243	243	243	243	243	243	243	243
22	22	22	22	21	21	20	23	22	18	23	22	18	23	23	22	22	22	23	22	22	22	22	22	22	22	22	23	22	21	22	22	22	22	22
AAB49598	S	AAB65828	AAE05529	AAY71035	AAB30233	AAY21807	ABB08221	AAE05527	AAW09108	ABB08222	AAE05528	AAW09107 .	ABB80582	ABB80583	ABG12723	AAB65824	AAB65819	AA021663	ABG12724	AAB65821	AAB65896	AAB65898	AAB65897	AAB65899	AAB65816	AAB65820	ABB72179	AAB55979	AAY76040	AAB65890	AAB65889	588	859	AAB49599
Human ACRP30 prote	Human ACRP30 prote	Human adipocyte co			Human adipocyte co		adipo	Mouse OBG3 protein	¥	Mouse acrp30 prote	Mouse OBG3 protein	Murine adipocyte c	Human sbg1033026C1	Human sbg1033026C1	Novel human diagno	Murine TANGO 253 C	Human TANGO 253 C1		_		Murine secreted pr	secreted	secreted	secret	TANG	ine TANGO	protei	n cell prot	kin cell p	_	secreted	secreted	secreted p	Human adipocyte co

## ALIGNMENTS

RESULT 1
AAY06481
ID AAY0
XX
AC AAY0
XX

AAY06481 standard; Protein; 243 AA

AAY06481

Human tumour-associated 27-SEP-1999 (first entry)

protein PRO344

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PXPXPXT
                                                                                                                                                                                    20-NOV-1998;
05-JAN-1998;
29-APR-1998;
                                       05-JAN-1999;
                                                                                                                                                                                                             PRO344; UNQ303; cancer; tumour; diagnosis; therapy; human.
                                                        15-JUL-1999
                                                                           W09935170-A2
                                                                                                        Modified-site
                                                                                                                                             Protein
                                                                                                                                                                          Key
                                                                                                                                                                                            Homo sapiens
                                                                                                                          Modified-site
                                                                                                                                                               Peptide
98US-0109304.
98US-0070440.
98US-0083500.
                                       99WO-US00106
                                                                                                       /note- "N-myristoylated" 216..243
                                                                                                                          /note= "mature protein" 68..215
                                                                                                                                             /note= "signal peptide"
16..243
                                                                                                                                                                        Location/Qualifiers
                                                                                              /note= "N-myristoylated"
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Best Local Similarity
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10-JUN-1998;
10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents human PRO344 (UNQ303), a protein encoded by the novel cDNA clone DNA40592 (see AAX87258). Amplification of DNA40592 was observed in primary lung tumours and in primary colon tumours, suggesting a significant role in tumour formation and growth. Antagonists (e.g. antibodies) directed to PRO344 may have use in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour cells. Such amplification is expected to be associated with overexpression of the gene product and to contribute to tumorigenesis. The encoded proteins (see AAY06477-90) may be useful targets for the diagnosis and/or treatment (including prevention) of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies that bind the proteins are claimed and used in claimed cancer
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1;
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                                                                    12-AUG-1999
                                                                                        AAY17827;
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                                               Human PRO344 protein sequence
                   secreted protein;
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DB; AAX87258.
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                             PRO protein; tumour necrosis factor family; TNF;
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Wood WI;
                                                                                                                                                                                                                                                                                standard;
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                                                                                                                                                                                                             FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
                                                                                                                                                                                                                                                   APLPEDRVLVNEQGHYDAVTGKETCQVPGVYYFAVHATVYRASLQEDLVKNGESIASFFQ
                                                                                                                                                                                                                                                                                                                                            MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
                                                                                                                                                                                                   FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
                                                                                                                                                                                                                                         APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
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                                                                    (first entry)
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98US-0088742.
98US-0107783.
                  transmembrane protein; inflammation disorder.
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                                                                                                           Protein; 243
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Pred. No. 5.3e-103;
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                             cytokine;
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Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12;
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N-PSDB; AAX80052.
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09-FEB-1998
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17-DEC-
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03-DEC-1997;
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VFA
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                                                                                                                                                                                         APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                           VFA 243
                                                       FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
                                                                                                                                                                           APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
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                                                                                                                                                                                                                                                                                                                                                        243 AA;
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98US-0074092
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97US-0069870
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Pred. No. 5.3e-103;
); Mismatches 0;
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collagen-like domain capable of dimerisation or oligomerisation. zsig39 polypeptides were initially identified by querying an EST database for secretory signal sequences characterised by an upst
                        This polypeptide comprises human adipocyte-specific protein a protein that modulates free fatty acid metabolism. zsig39 member of a family of proteins having a globular domain and
                                                           Claim
                                                                                                                                                                                                                                   Doma in
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                                                                                                                                      (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                        26-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
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                                                                                                    1999-204665/17.
                                                         1; 111-112; 132pp; English.
                                                                           protein - used to modulate fatty acid metabolism
                                                                                            AAX24684
                                                                                                                     Sheppard
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187..20
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164..1
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Best Local Similarity
Matches 243; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           radionuclectides, enzymes or fluorophores, fusion proteins including zsig39 polypeptides, an antibody that specifically binds to an epitope of zsig39, and a method for modulating free fatty acid metabolism by administering a zsig39 polypeptide. The zsig39 polypeptide may also be used in organ preservation, for cryopreservation, for surgical pretreatment to prevent injury duto ischaemia and/or inflammation, and as an antimicrobial agent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           method of producing zsig39 polypeptide are claimed, as well as zsig39 polypeptides having N- or C-terminal affinity tags, toxins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein apM1. A full lung tissue library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adipocyte complement related protein Acrp30 and adipocyte secreted protein apM1. A full-length clone (see AAX24684) was obtained from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acids and a cleavage site. A single EST sequence was discovered, and the novel polypeptide encoded by the full-length cDNA allowed the identification of a homologue relationship with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methionine start site,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoting
AAB33461 standard;
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                                                                                                                                         APLPEDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQEDLVKNGESIASFFQ
                                                                                                                                                                                                                                                                                                                                                    WRPLLVLLLIGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
                                                                                                            VFA 243
                                                                                                                                                                                                                                                                                        APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                              VFA 243
                                                                                                                                                                                                          APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
                                                                                                                                                                                                                                                                        APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                                                                                                                                                                                                                                                     MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lysis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 .AA;
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phagocytosis of infectious agents.
 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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 243
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1325; DB 20;
Pred. No. 5.3e-103;
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                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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injury due
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AAB33461;

29-JAN-2001 (first entry)

Human PRO344 protein UNQ303 SEQ ID NO:241

antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syntome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune thrombocytopaenia; immune-mediated renal disease; demyelinating disease; hepatobiliary disease; Whipple's disease; inflammatory bowel disease; jluten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; allergic disease; autoimmune disease; immune-mediated skin disease; allergic disease; autoimmune disease; immune-mediated skin disease; allergic disease; Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective; antianaemic; hepatotropic; virucide; antipsoriatic; antialiergic; antianaemic; hepatotropic; virucide; antipsoriatic; antialiergic; immunological disease; transplantation asso graft rejection; graft-versus-host-disease. associated disease;

sapiens.

WO200053758-A2

attable from Albert

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proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erthematous, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, and the contraction of the contractions of the contraction
                                                                                                                                                                                                                                                                                                                                             Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
                                                                                                                                                                                                                                  The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO
                                                                                                                                                                                                                                                                                                          Claim 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-DEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kabakoff RC,
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2000WO-US00277.
2000WO-US00376.
2000WO-US03565.
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2000WO-US04342.
2000WO-US04414.
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Pan J, Pennica
, Watanabe CK,
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                                                                                                                                                                                                                                                                                                     English.
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D, Shelton DL,
Wood WI, Yan M;
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DL, Smith
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immune-mediated

01-DEC-1998;

98WO-US25108

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local
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                                                      30-NOV-1999;
                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour breast; prostate; colon; lung; renal; ovarian; central nervous system; CNS; leukemia; melanoma; Expressed Sequence Tag; EST; secreted protein; extracellular domain; ECD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AAC58397 to AAC58578 represent PCR primers and hybridisation probes in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
                                                                                                    08-JUN-2000
                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY71468 standard;
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                                                                                                                                                                                                                                                                          Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO344 protein.
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68..74
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16..24?
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11..17
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                                                                                                                                                                                                                                                /note= "Cell attachment sequence"
                                                                                                                                                                                                    'note-
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Pred. No. 5.3e-103;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Sir
Matches 243;
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is the human PRO344 protein, encoded by the cDNA clone, designated as DNA40592-1242. It is isolated from human foetal lung tissue, cDNA library, identified using probes based on a consensus sequence DNA34398, derived from secreted protein extracellular domain (ECD) expressed sequence tag (EST). This clone is assigned ATCC deposit No: 209492. PRO344 functions as a neoplastic cell growth inhibitor and is used for treating tumours, using an effective amount of PRO655, PRO364 and PRO344. This composition is especially useful for treatment of human cancers such as breast, prostate, colon, lung, renal, ovarian and CNS, levitoris and molarcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen
                                                                                                                                AAY93688 standard; Protein;
                  Homo sapiens
                                                                        Amino acid sequence of novel polypeptide PRO344.
                                                                                              03-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 31; Fig 6; 108pp;
                                     tumourigenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New composition useful for inhibiting neoplastic cell growth and for treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or
                                                                                                                                                                                                                                                                                                                                                                                                                                      leukemia
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22-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-412325/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ing cancers, comprises antagonists -
                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                     61
                                            PRO322; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cel
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENENTECH INC.
                                                                                                                                                                                                                                                          APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                                                                                                                                                                                                                                                               MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                      and melanoma.
                                                                                                                                                                                 VFA 243
                                                                                                                                                                                                    VFA 243
                                                                                                                                                                                                                                                                                                 APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                                                                                                                                                                                                                                                      MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
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                                                                                                                                                                                                                                                                                                                                                                                                                    243 AA;
                                                                                                                                                                                                                                                                                                                                                                            100.0%;
ilarity 100.0%;
Conservative
                                                                                          (first entry)
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98US-0113296.
99US-0144758.
99US-0145698.
                                  cancer; neoplastic cell growth; cell proliferation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                  243 AA
                                                                                                                                                                                                                                                                                                                                                                           Score 1325; DB 21;
Pred. No. 5.3e-103;
D; Mismatches 0;
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Best Local
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30-NOV-1999;
01-DEC-1999;
02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                       Botstein Wood WI;
                                                                                                                                                                                                   Sequence
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02-JUN-1999;
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DB; AAA46907.
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                                                                                                                                                                      Similarity
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                                                                                                                                                                                                   243 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
11..17
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The present sequence represents a novel human polypeptide. The specification describes novel polypeptides designated PRO201, PRO292, PRO327, PRO1265, PRO344, PRO343, PRO347, PRO357, PRO1117, PRO1112, PRO293, PRO853 and PRO882. These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumourigenesis. The polypeptides are useful target for the identification of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies against these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth and proliferation of reatment and diagnosis of neoplastic cell growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 61; Fig 10; 220pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New anti-polypeptide antibody useful in the treatment and diagnosis neoplastic cell growth and proliferation - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proliferation in mammals.
APLPEDRYLVNEQGHYDAVTGKETCQVPGVYYFAVHATVYRASLQEDLVKNGESIASEFQ
                                                                                                                                                                                                APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                                                                                                                                                                                MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGAPG
                                                                                                                                                                                                                                                                                    MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
                                                                                                                                                                          APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                   APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
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99WO-US28301.
99WO-US28565.
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99WO-US21090.
99WO-US28313.
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99WO-US12252
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216..222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "N-myristoylation 68..74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "N-myristoylation 77..80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "signal peptide"
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                                                                                                                                                                                                                                                                                                                                                    0;
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Pred. No. 5.3e-103;
; Mismatches 0;
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Query Match
Best Local Similarity
Matches 243; Conserv
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16-DEC-1998;
22-DEC-1998;
                                                                                                   polypeptides which are designated as PRO polypeptides are described the membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243; PRO715; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347; PRO355; PRO361; PRO365; transmembrane polypeptide; PRO359; screening; detection; inhibition; probe; primer; human
                                                                     Sequence
                                                                                                                                                                                                                           New human nucleic acids encoding secreted and transmembrane
                                                                                                                                                                                                                                                         Claim 12; Fig 18; 187pp; English.
                                                                                                                                                                                                                                                                                                           New human nucleic acids encoding secreted and transmembrane polypeptides, designated as PRO polypeptides, useful as pharmaceutical
                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-412324/35.
N-PSDB; AAA49560.
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Hillan KJ, K
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                                                                                                                                                                                                                                                                                           diagnostic agents
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                                                                                                                                                                                                                                                                                                                                                                                                             Botstein D, Ea
ME, Goddard A,
, Kljavin IJ, N
                                                                     243 AA;
   Conservative
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98US-0112850.
98US-0113296.
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68..74
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77..80
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                 100.0%;
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1, Godowski PJ, Grimaldi CJ, Gurn
Napier MA, Roy MA, Tumas D, Woo
 0;
Score 1325; DB 21; Pred. No. 5.3e-103; Mismatches 0;
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                                 Length 243;
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 RESULT 8
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24-FEB-2000;
01-MAR-2000;
20-MAR-2000;
21-MAR-2000;
30-MAR-2000;
17-MAY-2000;
22-MAY-2000;
02-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secretory and transmembrane; PRO; mammallan; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alcartilage; ear; proliferation; glucose; free fatty acid; skelett adipocyte; A-peptide; factor VIIA; gene therapy.
                                                                                                                                                                                                                                                                                                                                             16-DEC-
20-DEC-
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01-DEC-1999;
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02-DEC-1999;
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Human TANGO 253 SEQ ID NO:
                                                       28-MAR-2001
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Goddard A, Godowski PJ, Gurney AL, Sherwood S;
art TA, Tumas D, Watanabe CK, Wood WI, Zhang Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The
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                                                                                                                                                                    Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                             the protein and coding sequences of human and murine secreted or transmembrane proteins TANGO 253, TANK TANGO 281 and INTERCEPT 258. These are useful in the treatment of coronary, pulmonary, olfactory, immunological, neurological, developmental and kidney disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                  Human adipocyte complement related protein homolog zsig39
                                         13-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acids for treating diseases and disorders, e.g. atherosclerosis, infection, autoimmune diseases, obesity, ear disorders, brain disorders, tumors, diabetes, arthritis, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; mouse; secreted protein, ....... disorder; InTERCEPT 258; coronary disorder; olfactory disorder; neurological disorder; pulmonary disorder; immunological disorder; developmental disorder; kidney disorder.
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                                                                                                                                                                                                                                                                     APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
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Pred. No. 5.3e-103;
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Human; zacrp5; gene therapy;

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inhibition; Clq domain;

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel adipocyte complement related protein homolog, ZACRP5, useful for diagnosing and treating inflammation, vascular injury microbial infections, and in wound healing -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 1; 121pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein. This protein was used in a sequence homology alignment with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zacrp5 protein and coding sequence (see AAB49590 and has a carboxyl-terminal Clq domain. The zacrp5 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1325; DB 22;
Pred. No. 5.3e-103;
; Mismatches 0;
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RESULT 11 AAB49599

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                                                                                                                                                                                                                                                                                                      The present invention relates to human adipocyte complement related protein homolog, ZACRP6 protein and coding sequence (see AAB89596 and CC AAC90051). ZACRP6 has a carboxyl-terminal Clq domain. The zacrp6 gene is located on human chromosome 21q. zacrp6 gene and protein are useful for cd diagnosing and treating inflammations, for determining arterial cremodelling, for modulating calcium ion concentration, hormone secretion, DNA synthesis or cell growth, inositol phosphate turnover, arachidonate release, phospholipase C activation, gastric emptying, human centrophil activation or ADCC capability and superoxide anion production. Target gene and protein are also useful as antimicrobial applications, preferably against bacteria and virus, for complement inhibition, for treating acute vascular injury, disseminated intravascular coagulation, arteriosclerosis and for wound healing. The present sequence is human adipocyte complement related protein homolog zsig39. This protein was used in a sequence homology comparison with ZACRP6 protein.
                                                                                                                                                                                                                         Query Match
Best Local S
Matches 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel adipocyte complement related protein homolog, ZACRP6, useful as modulators of neurotransmission and for treating disseminated intravascular coagulation, arteriosclerosis and acute vascular injury
                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 119pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wound healing; zsig39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB49599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB49599 standard; Protein;
                                                                          19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adipocyte complement related protein homolog
                                                                                                                                                                                                                                             Similarity
                     APLPEDRVLVNEQGHYDAVTGKETCQVPGVYYFAVHATVYRASLQEDLVKNGESIASFEQ
                                                                                              APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                                                                                    MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGRDGAPG
                                                                          APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                                                                 MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
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                                                                                                                                                                                                                         100.0%; Score 1325; DB 22; 100.0%; Pred. No. 5.3e-103; tive 0; Mismatches 0;
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RESULT 12
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Best Local Similarity
Matches 242; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides the protein and coding sequences of the human and murine secreted or transmembrane proteins TANGO 253, TANGO 27 TANGO 281 and INTERCEPT 258. These are useful in the treatment of coronary, pulmonary, olfactory, immunological, neurological, developmental and kidney disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281; INTERCEPT 258; coronary disorder; olfactory disorder; neurological disorder; pulmonary disorder; immunological disorder; developmental disorder; kidney disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acids for treating diseases and disorders, e.g. atherosclerosis, infection, autoimmune diseases, obesity, ear disorders, brain disorders, tumors, diabetes, arthritis, multiple sclerosis and asthma
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FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
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Pred. No. 7.8e-103;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acids for treating diseases and disorders, e.g. atherosclerosis, infection, autoimmune diseases, obesity, ear disorders, brain disorders, tumors, diabetes, arthritis, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281; INTERCEPT 258; coronary disorder; olfactory disorder; neurological disorder; pulmonary disorder; immunological disorder;
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VFA 243
                                                   McKay C,
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Pred. No. 1.1e-102;
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Matches 242;
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Pred. No. 1.1e-102;
0; Mismatches 1;
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human and murine secreted or transmembrane proteins TANGO 253, TANTANGO 281 and INTERCEPT 258. These are useful in the treatment of coronary, pulmonary, olfactory, immunological, neurological, developmental and kidney disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences of the human and murine secreted or transmembrane proteins TANGO 253, TANGO 257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acids for treating diseases and disorders, e.g. atherosclerosis, infection, autoimmune diseases, obesity, ear disorders, brain disorders, tumors, diabetes, arthritis, multiple
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                                                 FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
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Pred. No. 1.1e-102;
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Search completed: June 18, 2003, 14:51:05 Job time: 87 secs

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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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(without alignments)
618.141 Million cell updates/sec
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09d8u4 mus musculu
095j95 canis famil
09d2v4 mus musculu
0921s8 mus musculu
096d07 homo sapien
08tej5 homo sapien
09dcm6 mus musculu
0920n0 tamias sibi
0919q7 carassius a
0919q9 cyprinus ca
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Q95mq4 bos taurus
Q95jd7 macaca mula
Q9n178 sus scrofa
Q9zlk4 rattus norv
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45	44	43	42	41	40	39	38	37	36	ω S	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.5	16.6	16.6	16.6	16.6	16.6	16.6	16.7	16.7	16.8	16.8	16.8	16.8	17.0	17.7	17.7	17.9	18.0	18.0	18.0	18.2
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## ALIGNMENTS

QY 61 AFGEKGGGRFGLFGPRGDFGFRGEAGFAGFTGFAGECSVPPRSAFSAKKSESRVPPPSD 120	Best Local Similarity 93.4%; Pred. No. 5.1e-100; Best Local Similarity 93.4%; Pred. No	SEQUENCE FROM N.A.  Strausberg R.;  Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.  EMBL; BC023068; AAH23068.1;  EMBL; BC025174; AAH25174.1;  EMBL; BC025174; AAH25174.1;  Hypothetical protein.  SEQUENCE 243 AA; 25420 MW; 498129CD051DB97B CRC64;	RESULT 1  QBR002 PRELIMINARY: PRT; 243 AA.  ID QBR002 PRELIMINARY: PRT; 243 AA.  AC QBR002;  DT 01-JUN-2002 (TrEMBLrel. 21, Created)  DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  DE Similar to DKFZP596B0621 protein (Hypothetical 25.4 kDa protein).  OS Mus musculus (Mouse).

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RESULT
Q95JD7
ID Q9
AC Q9
DT 01
DT 01
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InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 1.
ProDom; PD000007; Collagen; 1.
PROSITE; PS01113; C10; UNKNOWN_1.
SEQUENCE 240 AA; 26091 MW; C62
       01-DEC-2001
01-DEC-2001
01-JUN-2002
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 21, Last annotation update)
01-DUN-2002 (TrEMBLrel. 21, Last annotation update)
Adipose tissue-specific protein adipo Q.
Bos taurus (Bovine). Chordata; Craniata; Vertebrata; Eutel Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID-9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein, Adipo Q.";
J. Biol. Chem. 276:28849-28856(2001).
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Sato C., Yasukawa Z., Honda N., Ma
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2 (TrEMBLrel.
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                                                         Created)
       Last sequence update)
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                                                                                                          PRT;
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Best Local :
                                                                                                                                                                                                                        Sus scrofa (Pig).
Eukaryota; Metazoa; (
Mammalia; Eutheria; (
NCBL_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                            Q9N178
Q9N178;
Q1-OCT-2000
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Hansen B.C., Matsuzawa Y.;
"Circulating concentrations of the adipocyte protein adiponectin
decreased in parallel with reduced insulin sensitivity during the
progression to type 2 diabetes in rhesus monkeys.";
Diabetes 50:1126-1133(2001).
EMBL; AR404407; AAK92202.1;
InterPro; IPR001073; CO1,
InterPro; IPR001073; CO1,
InterPro; IPR001073; CO1,
Pfam; PP01391; CO1lagen.
Pfam; PP01391; CO1lagen.
                                                                                                SEQUENCE FROM N.A.
MEDLINE=21015405; PubMed=11130976;
Nielsen V.H., Bendixen C., Arnbjer
Shukri N.M., Thomsen B.;
"Abnormal growth plate function in type X collagen.";
Mamm. Genome 11:1087-1092(2000).
EMBL; AF222861; AAF37271.1;
                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                              COLIOA1.
                                                                                                                                                                                                                                                                                                                                                   Type X collagen.
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MEDLINE-21232234; Pubm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                                       Arnbjerg
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Last annotation update)
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Pred. No. 1
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was and

118

Pfam; PF00386; C1q; 1. Pfam; PF01391; Collagen; 8. InterPro; IPR001073; Clq. InterPro; IPR000087; Collagen

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RESULT 5

Q221K4

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Best Local S
Matches 94
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                                                                                                                                        Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 3.
PRINTS; PR00007; COMPLEMNTC1Q.
SMART; SM00110; C1Q; 1.
PROSITE; PS011113; C1Q; 1.
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Q921K4;
                                                                                                                                                                                                                                                                                                                    failures of chondrocyte patterning and type Int. J. Dev. Blol. 44:309-316(2000). EMBL; AJ131848; CAA10518.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-SPRAGUE-DAWLEY;
MEDLINE-20310874; PubMed-10853827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Rat
NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                              InterPro: IPR001073; C1q.
InterPro: IPR000087; Collagen.
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  Local 94;
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ProDom; PD000007; Collagen; 2.
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    462 GFPGSKGDPGNPGPPGPAGIATKGLNGPTGPPGPPGPKGHAGEPGLPGPPGPPGPPGQ-A 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 GSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLP 74
                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity 36.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTDNDQVWLQLPNAGSNGLYSSEYVHSSFSGFLV 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGIFTCRIPGIYYFSYHIHVKGTHAWVGLYKNGTPVMYTYDEYVKGYLDQA--SGSAILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGKETCQVPGVYYFAVHATVYRASLQFDLVKNGESIA-SFFQFFGGWPKPASLSGGAMVR 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPP-----RSAFSAKRSESRVP------PPSDAPLPFDRVLVNEQGHYDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNPGLPGPKGDPGIGGPPGLPGPVGPAGAKGVPGHNGEAGPRGAPGIPGTRGPIGPPGIP
                                                                                                         295
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              675 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                         A,
                                                                                                         30012 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65447 MW;
                         30.3%; Score 402; DB 11; 36.7%; Pred. No. 9.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10, Created)
10, Last sequence update)
21, Last annotation update)
       31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 415.5;
Pred. No. 1.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                               FF43B1548028813E CRC64;
       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26397B10310383F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .7e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6;
       79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82;
                                                   Length 295;
       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 675;
  52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
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7;
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Matches

Conservative

Mismatches

Indels

44;

Gaps

6.

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ACOCO DITORNA CON CONTROL CONT
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Q9D8U4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Saki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Saki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Wattataker C., Wilming L.,
RA Wyonshaw-Roris A Yoshida W. Hasenawa Y Kawaii H. Kohtenki G., Willining L.,
RA Wyonshaw-Roris A Yoshida W. Hasenawa Y Kawaii H. Kohtenki G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ωy
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                                   Query Match
Best Local
                                                                                                                                                PRINTS; PRO0007; COMPLEMNTC1Q.
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
                                                                                                                                                                                                                                                InterPro; IPR001073; C1q.
InterPro; IPR0010087; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 2.
                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length Nature 409:685-690(2001).
EMBL; AK007683; BAB25187.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9D8U4;
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1916433; 1810033K05Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-PANCREAS;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 łayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9D8U4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1810033K05RIK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 PKGVPGHNGEAGPRGEPGIPGTRGPIGPPGIPGFPGSKGDPGKPGAPGPAGIVTKGLNGP 100
                                   Similarity
                                                                                                                             ; PS01113; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IYASIKTDSTFSGFLV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYYRASLQFDLYKNG-ESIASFFQFFGGWPKPASLSGGAMYRLEPEDQYWYQYGYGDYIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTGMPVSAFTVILSKAY--PAVGAPIPFDEILYNRQQHYDPRSGIFTCKIPGIYYFSYHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----PRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGRPGLPGPR---GDPGPRGEAGPAGPTGPAGECSVP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HVKGTHVWVGLYKNGTPTMYTYDEYSKGYLDQA--SGSAIMELTENDQVWLQLPNAESNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGPPGRPGPRGHTGEPGLPGPPGPPFGPPSQAVIPDGFTKSGQRPRLSGMPLVSANQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30865 MW;
                                29.8%; Score 395; 35.9%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17,
17,
                                Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                   6D3905AE7C19E6FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294
DB 11;
3.7e-26;
nes 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse cDNA collection. ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ŗ
                                                         Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218
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Query Match
Best Local
                                                                                                                                                                                                                                                                                                    Matches
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095J95; PRELIMINARY; PRT; 194 AA.
095J95; Preliminary; Prt; 194 AA.
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
Probom; Pb000007; Collagen; 1.
PROSITE; PS01113; ClQ; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kabir M., Ananthnarayan S., Ionut V., Kim S.P., Van Citters G.W., Dea M.K., Bergman R.N.;
"Regulation of Adiponectin gene expression in the fat-fed dog.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AF417206; AAL09702.1;
InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-ADIPOSE TISSUE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-9615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adiponectin
                                                                               103
                                             178
                                                                                                                   118
           160
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                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                        PSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIAS
       LFTYDQYQEKNVDQASGSVLLHLEVGDQVWLQV 192
                                       FFQFFGGWPKPA-SLSGGAMVRLEPEDQVWVQV 209
                                                                                                                                            EKGDPGLVGPKGDTGETGVTGVEGPRGFPGTPGRKGEPGESAYVHRSAFSV-GLESRITV
                                                                                                                                                                                EGGRPGLPGPRGD-------PGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPP
                                                                                                                                                                                                                    VLLPLPKGA------CPGWMAGIPGHPGHNGT---PGRDGRD-----GTPGEKG
                                                                                                                                                                                                                                           LLLGLAAGSPPLDDNKIPSLCPG-HPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKG
                                                                          P-NVPIRETKIEYNLQNHYDGTTGKEHCNIPGLYYESYHITVYLKDVKVSLYKKDK--AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGI-YASIKTDSTESGELVYSD 235
|: | || || |:||:|:|
NGLEYDPYWTDSLETGELIYAD 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YDITLANKHLAIGLVHNGQYRIRTFDANTGNHDVA--SGSTILALKEGDEVWLQIFYSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEEGPPGRTGNRGKQGPKGKAGAIGRAGPRGPKGVSGTPGKHGTPGKKGPKGKKGEPGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEKGEGGRP---GLPGPRGDPGPRGEAGPAGP---TGPAGECSVPPRSAFSAKRSESRVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPSDA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPCSCGSSRAKSAFSVAVTKSYPRERLPIKEDKILMNEGGHYNASSGKFVCSVPGIYYFT
                                                                                                                                                                                                                                                                                                                                                                         194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment).
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                      194
20890 MW; 3AA3D947D187AF9A CRC64;
                                                                                                                                                                                                                                                                                                            28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------PLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFA 154
                                                                                                                                                                                                                                                                                               Score 373.5; DB 6;
Pred. No. 1.6e-24;
2; Mismatches 66;
                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                               194;
                                                                                                                                                                                                                                                                                             35;
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                            177
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kidota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Havashiyaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00386; Clg; 1.
Pfam; PF01391; Collagen; 7.
PRINTS; PR00007; COMPLEMNTCIQ.
SMART; SM00110; ClQ; 1.
PROSITE; PS01113; ClQ; 1.
SEQUENCE 744 AA; 73581 MW; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9D2V4 PRELIMING...,
Q9D2V4;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AKO18742; BAB31383.1;
MGD; MGI:88463; CO18a1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001073; C1q. InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21085660;
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                                    205
                                                                        656
                                                                                                                                                                                                                                                                               476 VPGLLGPKGEPGIPGDQGLQGPPGIPGIVGPSGPIGPPGIPGPKGEPGLPGPPGFPGVGK 535
                                                                                                                                                                                                                                                                                                                     24 IPSLC--PGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLP-----
                                                                                                                                                                                                                                                                                                                                                             93;
                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                     QVPGVYYFAVHATVYRASLQFDLVKNGESIA-SFFQFFGGWPKPASLSGGAMVRLEPEDQ
VFLQMPSEQAAGLYAGQYVHSSFSGYLLY
                              VWVQVGVGDYIGIYASIKTDSTFSGFLVY 233
                                                                EVPGVYYFAYHVHCKGGNVWVALFKNNEPMMYTYDEYKKGFLDQA--SGSAVLLLRPGDQ
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                         28.0%; Score 370.5; DB 34.6%; Pred. No. 1.4e-23
                                                                                                                                                                                                                                                                                                                                                           32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                C659BDCCBCD6EB9C CRC64;
                                                                                                                                                                                                                                                                                                                                                             Mismatches
742
                                                                                                                                                                                                                                                                                                                                                                                            DB 11;
                                                                                                                                                                                                                                                                                                                                                           83;
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Q96D07 10 Q96D0 AC Q96D0 AC Q96D0 DT 01-DE DT 01-JU DE Hypot OS Homo OC Eukar OX NCBI_RN [1] RP SEQUE RC TISSU RA Strau RL Submil DR Inter DR Inter DR Inter DR Ffam;
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Q92158
ID 2169
AC Q9
DT Q101
DT Q1

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Best Local
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                                                                                                                                                                                                                        Q96D07 PRELIMINARY; PRT; 744 AA.
Q96D07;
Q96D07;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 21, Last annotation update)
Hypothetical 73.4 kDa protein.
Hypothetical 73.4 kDa protein.
Hypothetical 73.4 kDa protein.
Exprayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC013581; AARH3581.1; -.
InterPro; IPR001073; C1q.
InterPro; IPR000087; C01lagen.
                                                                                                                                             TISSUE-LUNG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 7.
PROSITE; PS01113; C1Q; UNKNOWN_1.
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                   NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001
01-DEC-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (JUL-2001) to the
EMBL; BC011061; AAH11061.1;
MGD; MGI:88463; Col8a1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 IPSIC--PGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VWVQVGVGDYIGIYASIKTDSTFSGFLVY 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVPGVYYFAYHVHCKGGNVWVALFKNNEPMMYTYDEYKKGFLDQA--SGSAVLLLRPGDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KPPHAYAGKKGKHGGPAYEMPAFTAELTVPFPPVGAPVKFDKLLYNGRQNYNPQTGIFTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGVAGLHGPPGKPGALGPQGQPGLPGPPGPPGPPGPPAVMPTPSPQGEYLPDMGLGIDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPRSAFSAKR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VFLQMPSEQAAGLYAGQYVHSSFSGYLLY 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----AGECSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VPGLLGPKGEPGIPGDQGLQGPPGIPGIVGPSGPIGPPGIPGPKGEPGLPGPPGFPGVGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           744 AA;
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1 (TrEMBLrel.
2 (TrEMBLrel.
n, type VIII,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73621 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.0%; Score 370.5; DB 1 34.6%; Pred. No. 1.4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----SESRVP-PPSDAPLPFDRVLVNEQGHYDAVTGKFTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 19, Created)
. 19, Last sequence upd
. 21, Last annotation u
, alpha 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF7A7FD79D8463AA CRC64;
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thi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ⋧
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on update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       713
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DR
SQ
                                                                                                                                                                              Matches
                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                        Q8TEJ5 PRELIMINARY;
Q8TEJ5;
01-JUN-2002 (TEMBLER: 21, C
01-JUN-2002 (TEMBLER: 21, L
01-JUN-2002 (TEMBLER: 21, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                     Submitted (JAN-2002) to the EMBL; AK074129; BAB84955.1; NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01391; Collagen; 7.
ProDom; PD000007; Collagen; 2.
PROSITE; PS01113; C1Q; UNKNOWN_1.
Collagen; Hypothetical protein.
Collagen; Hypothetical protein.
SEQUENCE: 744 AA; 73364 MW; 2BC1B0955DE2C9A3
                                                                                                                                                                                                                                                                        spleen."
                                                                                                                                                                                                                                                                                                        TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                         FLJ00201
                                                                                                                                                                                                                                                                                                                                                                                                 FLJ00201 protein (Fragment)
                                                                                                                                                                                                                                                                             Jikuya H., Takano J., Nomura N., Kikuno
The nucleotide sequence of a long cDNA
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11
                                                                                                                                                                                         Local
                  172
                                                                                                                           468 GLQGPAGPIGPQGLPGL-KGBPGLPGPPG-BGRAGEPGTAGPTGPPGVPGSPGITGPPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 QVWVQVGVGDYIGIYASIKTDSTFSGFLVY
:|::|: | :|| | :|||:||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            595
                                                                                               11 GLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           535
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                                                                                                                                                                              95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 IPSLC--PGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLP-----
                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90;
G-ESIASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGF
                                  ---PFPASGMPVKFDRTLYNGHSGYNPATGIFTCPVGGVYYFAYHVHVKGTNVWVALYKN
                                               SRVP-PPSDAPLPEDRVLVNEQGHYDAVTGKETCQVPGVYYFAVHATVYRASLQEDLVKN
                                                                            PGPPGPPGAPGAFDETG TAGLHLPNGGVEGAVLGKGGKPQFGLGELSAHATPAFTAVLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKPPHAYGAKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRQNYNPQTGIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVFLQMPSEQAAGLYAGQYVHSSFSGYLLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYDEYKKGFLDQA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CQVPGVYYFAVHATVYRASLQFDLVKNGESIA-SFFQFFGGWPKPASLSGGAMVRLEPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGVAGLHGPPGKPGALGPQGQPGLPGPPGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGIPGPKGEPGLPGPPGFPGIGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           705 AA;
                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                  Chordata;
Primates;
                                                                                                                                                                                                                       67430 MW;
                                                                                                                                                                        27.4%; Score 363.5; DB 4; 39.3%; Pred. No. 5.2e-23; Live 25; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.8%;
                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 368;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                      07DB85A65A948ED3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         705
                                                                                                                                                                                                                                                                              R., Nagase
clone isola
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.3e-23;
                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                        databases
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isolated
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                                                                                                                                                                                               Length 705;
                                                                                                                                                                         Indels
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                                                                                                     -GECSVPPRSAFSAKRSE
                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                    Homo
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from !
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                                                                                                                                                                        27;
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643

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RESULT 12
QDDCM6
QDDCM
AC QDDCM
AC QDDCM
DT 01-JU
DT 01-JU
DT 01-JU
DT COMPL
GN C1QA.
OS MUS m
OC EUKART
CO MAmma
OX NCBI
RA SEQUE
RA KAWAI
RA AIRAWA
RA AIRAWA
RA SAIto
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RA SAIto
RA KAWAI
RA SAIto
RA KAWAI
RA SICHT
RA KUCHI
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RA SICHT
RA KUCHI
RA KAWAI
RA SUCHI
RA CUSTRAI
RA GUSTRAI
RA GUSTRAI
RA GUSTRAI
RA HAYAS
RA SUZUM
RA HAYAS
RA HAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AR Kawai J. Shinagawa A. Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cosavant T.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Fesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Lyons P., Mafchionni L., Mashina J., Mazazarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Banawashi H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9DCM6;
Q9DCM6;
01-JUN-2001
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AK002655; BAB22262.1;
EMBL; BC002086; AAH02086.1;
MGD; MGI:88223; C1qa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000087; Collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001073; Clq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE+KIDNEY;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-C57BL/6J; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complement
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                                                                                                                                                                                                                                                                                                                                                                                'S; PR0007; COMPLEMNTC1Q.
f; SM00110; C1Q; 1.
ITE; PS01113; C1Q; 1.
ENCE 245 AA; 25974 MW;
           143 FTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWPKPA---
                                                                                  94
                                                                                                                                                                                           36
                                                                                                                                                                                                                                              29
                                                                                                                                                                                                                                                                                                 . Similarity
79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  701
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                                                                                                AGPTGPAGECSVP-----PRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGK 142
                                                           SGPOGLKGVKGNPGNIRDOPRPAFSAIRON---PMTLGNVVIFDKVLTNOESPYQNHTGR
                                                                                                                                                                    PGNPGRPGRPGLKGERGEPGAAGI--RTGIRGFKGDPGESGPPGKPGNVGLPGPSGPLGD
                                                                                                                                                                                                                       PGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLPGPRGDPGPRGEAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (JAN-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۲V
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                                                                                                                                                                                                                                                                                           Conservative
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
component 1, q subcomponent, alpha polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                         23.7%; Score 314; DB 11; 35.3%; Pred. No. 2.7e-19;
                                                                                                                                                                                                                                                                                     24;
                                                                                                                                                                                                                                                                                                                                                                                         41C2066D49592020 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                     85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          databases
                                                                                                                                                                                                                                                                                                                                   Length 245;
                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                36;
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                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                       93
                                                                                                                                                                                                                                                                             9
                                                                                                                                                              RESULT 14
Q920NO
        Baras
                                                                                                                                                                                                                                                                          В
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Best Local :
01-DEC-2001
01-DEC-2001
01-JUN-2002
HP-20.
                                                                                                           Q920N0
                                                                                                                                        Q920N0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0007; COMPLEMNTCIQ.
SMART; SM00110; C1Q; 1.
PROSTIE; PS01113; C1Q; 1.
SEQUENCE 246 AA; 26828 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding a putative secretory protein and its possible involvement skeletal development.";
J. Biol. Chem. 276:3628-3634(2001).

EMBL; AF246265; AAG33704.1;
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01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=21264842; PubMed=11071891;
Maeda T., Abe M., Kurisu K., Jikko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001073; Clq. InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             maeda T., Abe M., Kurisu K., Jikko A., I
"Molecular cloning and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collagenous recors or cors 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78;
                                                                                                                                                                                                                                                                                                                                                                                                            VKNGESIASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                    GFLLF 243
                                                                                                                                                                                                                                                                                                                     GFLVY 233
                                                                                                                                                                                                                                                                                                                                                                        MHNGNTVFSMYSYETKGKSDTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRVPPPSDAPLPEDRVLVNEQGHYDAVTGKETCQVPGVYYFAV----HATVYRASLQFDL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGNNGATGHEGAKGE-----KGDKGDLGPRGERGQHGPKGEKGYPGVPPELQIAFMASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGRDGAPGAPGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLPLLFLPFCLCQDEYMESPQAGGLPPDCSKCCHGDYGFRGYQGPPGPPGPPGIPGNHGN 70
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                   (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 AA;
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
repeat-containing sequence of 26kDa pro
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        Created)
Last sequence update)
Last annotation update)
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Pred. No. 1.5e-
33; Mismatches
                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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Best Local (
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Interpro; IPRO010087; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 1.
PROSITE; PS01113; C1Q; UNKNOWN 1.
SEOUENCE 196 AA; 21330 MW; B07D
InterPro; IPR000087; Collagen.
InterPro; IPR001304; Lectin_C.
Pfam; PF01391; Collagen; 2.
Pfam; PF00059; lectin_C; 1.
SMART; SM00034; CLECT; 1.
                                                                                                       WEDLINE-20456722; pubMed-11003389; Vitred L., Holmskov U., Koch C., Teisner B., Hansen S., Skjo The homologue of mannose-binding lectin in the carp family is expressed at high level in spleen, and the deduced primar structure predicts affinity for galactose. "; Immunogenetics 51:955-964(2000). EMBL; AF237739; AAF63470.1; -. HSSP; P35247; 1808.
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01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q919Q7
Q919Q7;
                                                                                                                                                                                                                                                                                                                                                                                                Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii;
Cyprinidae; Carassius.
                                                                                                                                                                                                                                                                                                          TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mannose binding-like lectin
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
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70; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGFLISS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPSE-PVVFTEVLYNTQRDLKASTGVFNCVEPGNYHFSFDVELYHCKVKIGLMKNHIQVM
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(TremBLrel 15, Last seq
(TremBLrel 21, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor (Fragment).
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                            ; Craniata; Vertebrata; Eu
Teleostei; Ostariophysi;
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67;
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i; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                  family Cyprinidae primary
                                                                                                                                                                                                                                                 Skjodt K.;
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Matches 80
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  195
                         228
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                                                                                                          119 SDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASF 178
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                                                                                                                                                                                              4 LLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGRDGAPGAPG
                                                                                                                                                                                                                                      80; Conserv
 TEGKQLTFTNW
                                                                                                                                                                                                                                                                                                                               Signal.
                                      MEF-----GGTMVSPRTSAENQALLKLVVSSGLGSKKPYIGV-TDRKTEGQFVD 194
                                                                                                                                                        EKGEG-----GRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPP
                                                                                                                                                                                                                                                                                                                                           PS00615;
PS50041;
                                                             FQFFGGWPKPASLSGGAMV--RLEPEDQVWVQV----GVGD---YIGIYASIKTDSTF--
                                                                                                                                  EKGESGVSVQGPPGKAGPPGTAGEKGERGPSGPQGSPGSESVLESLKSEIQQLKAKI---
                                                                                                                                                                                LLLQFALQLLDGAEPQNLN----CPAYGGVPGTPGHN---GLPGRDGRDGKDGAIGPKG
                      --SGFLVYSDW
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C_TYPE_LECTIN_2; 1.
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Pred. No. 5.2e-14;
3; Mismatches 73;
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Search completed: June 18, 2003, 14:52:31 Job time: 83 secs

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Maximum Match 100%
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536.617 Million cell updates/sec
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/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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US-09-944-92-42
US-09-944-92-42
US-09-944-92-362
US-10-121-049-362
US-10-140-470-362
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              42, Appl
362, Appl
TITLE OF INVENTION: ACIDS ENCODING TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PLC1
CURRENT APPLICATION NUMBER: U5/09/944,413
CURRENT APPLICATION NUMBER: U5/09/944,413
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
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US-09-944-413-42
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APPLICANT: Eaton, APPLICANT: Ferrararapplicant: Filvarapplicant: Gerritant
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Napier, Mary
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Tumas, Daniel
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Grimaldi, Christopher
Gurney, Austin
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Goddard, Audrey
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US-10-140-928-362
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US-10-123-903-362
US-10-123-903-362
US-10-124-819-362
US-10-124-822-362
US-10-124-925-362
US-10-160-498-362
US-10-160-498-362
US-10-121-041-362
US-10-121-043-362
US-10-121-043-362
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Best Local :
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SEQ ID NO 42
                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/06520 FILING DATE: February 28, 2001
                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                               FILING DATE: July 20 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US00/14042
FILING DATE: May 22, 2000
APPLICATION NUMBER: PCT/US00/20710
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PC
FILING DATE: March 30,
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FILING DATE: December1, 1999
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FILING DATE: No. US20020156004Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020156004Alember 30, 1999
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APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: 09/218,517
FILING DATE: December 22, 1998
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FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
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FILING DATE: December 16, 1998
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APPLICATION NUMBER: PCT/US98
FILING DATE: December 1, 1998
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APPLICATION NUMBER: 60/146,222
FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
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APPLICATION NUMBER: 60/074
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1 MRPLLVLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSOGLPGRDGRDGRDGAPG 60
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CATION NUMBER: PCT/US00/03565
G DATE: February 11, 2000
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llarity 100.0%;
Conservative 0;
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Pred. No. 2.3e-89;
Mismatches 0;
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CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: December 3, 1997
PRIOR PRIOR APPLICATION NUMBER: 60/069,334
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
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                             FILING DATE: December 18, 1997 APPLICATION NUMBER: 60/070,440
                                                           APPLICATION NUMBER: 60/068,017
                                                                                                                            APPLICATION NUMBER: 60/069,
                                                                                                APPLICATION NUMBER: 60/
                                                                                                                                                                                         APPLICATION NUMBER: 60/069,694
                                                                                                                                                                                                                          FILING DATE: December 12, 1997 APPLICATION NUMBER: 60/069,696
     APPLICATION
                     FILING DATE:
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APPLICATION NUMBER: 60/069,425
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FILING DATE: December 11, 1997
APPLICATION NUMBER: 60/069,278
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/944,403
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Tumas, Daniel
Wood, William
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Hillan, Kenneth
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: January 5, 19:
NUMBER: 60/074
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17, 1997
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; ORGANISM: Homo Sapien
US-09-944-403-42
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PRIOR FILING DATE: July 28, 1999
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OR FILING DATE: March 3, 1999
OR FIL
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APPLICATION NUMBER: PCT/US00/20710
FILING DATE: July 28, 2000
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APPLICATION NUMBER: PCT/US00/05841
FILING DATE: March 2, 2000
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APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020165143Alember 30,
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FILING DATE: No. US20020165143Alember
APPLICATION NUMBER: PCT/US99/28301
FILING DATE: December1, 1999
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FILING DATE: February 11, 2000
APPLICATION NUMBER: PCT/US00/04414
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FILING DATE: December 16, 1999
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APPLICATION NUMBER: 09/218,517
FILING DATE: December 22, 1998
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      FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP 240
                                                                                                                                                                                                    APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
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Pred. No. 2.3e-89;
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FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,896
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
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PRIOR FILING DATE: December 22, 1998
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PRIOR APPLICATION NUMBER: 60/112,
PRIOR FILING DATE: December 16, 1
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PRIOR APPLICATION NUMBER: 60/068
PRIOR FILING DATE: December 18,
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FILING DATE: December 17, 1997
APPLICATION NUMBER: 60/069,873
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APPLICATION NUMBER: 60/074,086
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Hillan, Kenneth
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TE: September 16, 1998
N NUMBER: PCT/VIS98/19330
E: Doc-
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181 121 Query Match Best Local S Matches 243

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SEQ ID NO 42

TYPE: PRT

LENGTH: 243

APPLICATION NUMBER: PCT/U999/12252
FILING DATE: June 22, 1999
APPLICATION NUMBER: PCT/US99/21090
FILING DATE: September 15, 1999

APPLICATION NUMBER: 0

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APPLICATION NUMBER: 09/218,517
FILING DATE: December 22, 1998
ADDITION NUMBER: 09/218,517

APPLICATION NUMBER:

09/216,021

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IOR APPLICATION UNMBER: PCT/US99/28409
IOR APPLICATION UNMBER: PCT/US99/28409
IOR APPLICATION NUMBER: PCT/US99/28313
IOR FILING DATE: NO. US20020168715A1ember 30, 1999
IOR APPLICATION NUMBER: PCT/US99/28301
IOR FILING DATE: NO. US20020168715A1ember 30, 1999
IOR APPLICATION NUMBER: PCT/US99/30095
IOR FILING DATE: December1, 1999
IOR APPLICATION NUMBER: PCT/US99/30095
IOR FILING DATE: December 16, 1999
IOR APPLICATION NUMBER: PCT/US90/03565
IOR FILING DATE: February 11, 2000
IOR FILING DATE: February 22, 2000
IOR APPLICATION NUMBER: PCT/US00/04414
IOR FILING DATE: March 2, 2000
IOR APPLICATION NUMBER: PCT/US00/08439
IOR APPLICATION NUMBER: PCT/US00/08439
IOR FILING DATE: March 30, 2000
IOR APPLICATION NUMBER: PCT/US00/14042
RIOR FILING DATE: MARCH 30, 2000
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CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR APPLICATION NUMBER: 60/069335
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
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APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PC1
FILE REFERENCE: P2548PC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: December
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/069, PRIOR FILING DATE: December 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/069,425 PRIOR FILING DATE: December 12, 1997
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                                                                                                                         OR FILING DATE: December 1, 1998
OR APPLICATION NUMBER: 09/216,021
OR FILING DATE: December 16, 1998
OR APPLICATION NUMBER: 09/218,517
OR FILING DATE: December 22, 1998
OR APPLICATION NUMBER: 09/254,311
OR FILING DATE: MATCH 3, 1999
OR APPLICATION NUMBER: PCT/US99/12252
OR FILING DATE: MATCH 3, 1999
OR APPLICATION NUMBER: PCT/US99/12252
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                                                                                                                                                                                                                                                                                                                                                                                                                                 OR FILING DATE: February 25, 1998
OR APPLICATION NUMBER: 60/112,850
OR FILING DATE: December 16, 1998
OR APPLICATION NUMBER: 60/113,296
OR FILING DATE: December 22, 1998
OR APPLICATION NUMBER: 60/146,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OR APPLICATION NUMBER: 60/0768,017
OR FILING DATE: December 18, 1997
OR APPLICATION NUMBER: 60/070,440
OR FILING DATE: January 5, 1998
OR APPLICATION NUMBER: 60/074,086
OR FILING DATE: February 9, 1998
OR APPLICATION NUMBER: 60/074,092
OR APPLICATION NUMBER: 60/074,092
OR APPLICATION NUMBER: 60/075,945
OR APPLICATION NUMBER: 60/075,945
OR FILING DATE: February 9, 1998
OR APPLICATION NUMBER: 60/075,945
                                                                 FILING DATE:
                                                                                   APPLICATION NUMBER:
                                                                                                               FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 6 FILING DATE: July 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gurney, Austin
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                                                      June 22, 1955
NIMBER: PCT/US99/21090
                                                                                                                                                                                                                                                                                                                                     NUMBER: PCT/US98/25108
                        September 15, 1999
NUMBER: PCT/US99/28409
                                                                                                                                                                                                                                                                                                                                                                September 16,
US20020173463A1ember 30,
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JS-09-944-944-42 GENERAL INFORMATION:
APPLICANT: Baker, K
APPLICANT: Botstel Sequence 42, Application US/09944944 Patent No. US20020173463A1 Baker, Kevin Botstein,David

В

181 181

241

VFA 243

241 VFA 243

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61

Query Match Best Local s Matches 243

Similarity

100.0%; ilarity 100.0%; Conservative 0

0.

Score 1325; DB 9; Pred. No. 2.3e-89; ); Mismatches 0;

hes 243;

LENGTH: 243 TYPE: PRT ORGANISM: Homo Sapien :-09-944-896-42

NUMBER OF SEQ ID NOS: SEQ ID NO 42

PRIOR FILING DATE: December 1, 2000 PRIOR APPLICATION NUMBER: PCT/US01/06520 PRIOR FILING DATE: February 28, 2001

FILING DATE: July 28, 2000 APPLICATION NUMBER: PCT/US00/32678

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US-09-944-907-42
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US-09-944-944-42
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 42, Applica Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 1325; DB 9; Best Local Similarity 100.0%; Pred. No. 2.3e-89; Matches 243; Conservative 0; Mismatches 0;
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APPLICANT:
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      PPLICANT:
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TYPE: PRT
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OR FILING DATE: MAICH 30, 2000
OR APPLICATION NUMBER: PCT/US00/14042
OR FILING DATE: MAY 22, 2000
OR APPLICATION NUMBER: PCT/US00/20710
OR FILING DATE: July 28, 2000
OR APPLICATION NUMBER: PCT/US00/32678
OR APPLICATION NUMBER: PCT/US00/32678
OR FILING DATE: DECEMBER 1, 2000
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FILING DATE: February 11, 2000
APPLICATION NUMBER: PCT/US00/04414
FILING DATE: February 22, 2000
APPLICATION NUMBER: PCT/US00/05841
FILING DATE: March 2, 2000
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APPLICATION NUMBER: PCT/US99/30095
FILING DATE: December 16, 1999
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                                                                                                                                                                                                                                                                                                                                                                                                   Baker, Kevin
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No. US20020198147A1
                                                                                                                                                                              Goddard, Audrey
Godowski, Paul
                                                             Kljavin, Ivar
                                                                                Hillan, Kenneth
                                                                                                                 Gurney, Austin
                                                                                                                                              Grimaldi, Christopher
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                         Napier, Mary
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NUMBER OF SEQ ID NOS:
SEQ ID NO 42
LENGTH: 243
                                                                                                                                                       TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1 CURRENT APPLICATION NUMBER: US/09/944,929 CURRENT FILING DATE: 2001-08-31
                                                                                                CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
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Roy, Margaret Tumas, Daniel Wood, William

POLYPEPTIDES

AND

NUCLEIC

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CURRENT APPLICATION NUMBER: US/09/944,907
CURRENT EILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
LENGTH: 243
TYPE: PRT
                                                                                                                                                                                                                                   RESULT 6
US-09-944-929-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo Sapien US-09-944-907-42
                                                                                                                                                                                          GENERAL INFORMATION
                                                                                                                                                                                                       Sequence 42, Application US/09944929 Publication No. US20020197612A1
APPLICANT:
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                                         APPLICANT:
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Best Local Similarity
                                                                                    APPLICANT:
                                                                                                                  APPLICANT:
                                                                                                                                                             APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
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                                                                                                                                                                                                                                                                                                                                                                                                                          APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYBASLQFDLVKNGESIASFFQ 180
                                                                                                                                                                                                                                                                                                                           VFA 243
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                                                      Godowski, Paul
Grimaldi, Christopher
Napier, Mary
             Kljavin, Ivar
                          Hillan, Kenneth
                                         Gurney, Austin
                                                                                    Goddard, Audrey
                                                                                                  Gerritsen, Mary
                                                                                                             Filvaroff, Ellen
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ilarity 100.0%;
Conservative (
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Pred. No. 2.3
0; Mismatches
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DATE: 1997-09-19

1997-09-24

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60/062814

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FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/028,072

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR FILING DATE: 1997-06-26

PRIOR APPLICATION NUMBER: 60/059113

PRIOR APPLICATION NUMBER: 60/059113

PRIOR APPLICATION NUMBER: 60/059115

PRIOR APPLICATION NUMBER: 60/059117

PRIOR APPLICATION NUMBER: 60/059117

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17
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US-09-944-929-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Baker, Kevin .P.
APPLICANT: Beresini, Maur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 362, Application No. US20 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Sin
Matches 243;
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION:
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         DR APPLICATION NUMBER: 60/059122
DR FILING DATE: 1997-09-17
DR APPLICATION NUMBER: 60/059184
DR FILING DATE: 1997-09-17
DR APPLICATION NUMBER: 60/059263
DR FILING DATE: 1997-09-18
DR APPLICATION NUMBER: 60/059352
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Watanabe, Colin K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stewart, Timothy A.
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DeForge, Laura
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ilarity 100.0%;
Conservative
1997-09-19
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Pred. No. 2.3e-89;
Mismatches 0;
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                 PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/077791
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PRIOR
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OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063045
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063082
OR FILING DATE: 1997-10-31
OR APPLICATION NUMBER: 60/063127
OR FILING DATE: 1997-10-24
OR PPLICATION NUMBER: 60/063327
OR FILING DATE: 1997-10-27
OR APPLICATION NUMBER: 60/063329
OR APPLICATION NUMBER: 60/063329
OR FILING DATE: 1997-10-27
OR APPLICATION NUMBER: 60/06350
OR FILING DATE: 1997-10-28
OR APPLICATION NUMBER: 60/063561
OR APPLICATION NUMBER: 60/063704
OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1997-11-03
APPLICATION NUMBER: 60/064809
FILING DATE: 1997-11-07
APPLICATION NUMBER: 60/065186
FILING DATE: 1997-11-12
                                                                     APPLICATION NUMBER: 60/
FILING DATE: 1998-02-09
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FILING DATE: 1997-12-16
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FILING DATE: 1997-12-11
APPLICATION NUMBER: 60/069278
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/066364 FILING DATE: 1997-11-21 APPLICATION NUMBER: 60/066453 FILING DATE: 1997-11-24
                                                                                                            FILING DATE: 1998-02-04
                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063738
FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063755
FILING DATE: 1997-10-17
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FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/062287
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FILING DATE: 1997-10-29
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FILING DATE: 1997-10-24
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APPLICATION NUMBER: 60
FILING DATE: 1997-10-1
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1998-03-

1998-01-23

60/074086 60/073612 60/072320 60/069694 60/069334

OR APPLICATION NUMBER: 60/081203
OR FILING DATE: 1998-04-09
OR FILING DATE: 1998-04-09
OR FILING DATE: 1998-04-09
OR APPLICATION NUMBER: 60/081695
OR FILING DATE: 1998-04-14

APPLICATION NUMBER: 60/ FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/079728 FILING DATE: 1998-03-27

60/080165

APPLICATION NUMBER: APPLICATION NUMBER:

1998-03-

60/079663 60/079294

LING DATE: 1998-02

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; ORGANISM: Homo Sapien US-10-121-049-362
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                                                                      Prior Application removed - See File Wrapper or NUMBER OF SEQ ID NOS: 550
SEQ ID NO 362
LENGTH: 243
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Best Local S
Matches 243
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 Query Match
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                                                                                                                             TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
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                                                          LENGTH: 24
TYPE: PRT
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OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090863
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091519
OR APPLICATION NUMBER: 60/091982
OR APPLICATION NUMBER: 60/091982
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Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                                                     Wood, William
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Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                                                                                                                                               Stewart, Timothy A
                                                                                                                                                                                                                                                                               Smith, Victoria
                                                                                                                                                                                                                                                                                             Sherwood, Steven
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100.0%;
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Pred. No. 2.3e-89;
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                                                                                                                                                                                         POLYPEPTIDES AND
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                                                                                                                  Palm
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OR FILING DATE: 1998-05-12
OR APPLICATION NUMBER: 60/085323
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085338
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085339
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085579
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085697

APPLICATION NUMBER: 60/084637 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/085149

FILING DATE: APPLICATION NUMBER:

1998-05-07

60/084627

APPLICATION NUMBER: 60/084600 FILING DATE: 1998-05-07

LING DATE: 1998-04-29

APPLICATION NUMBER: 60/083545

APPLICATION NUMBER: 60/083322 APPLICATION NUMBER: 60/082999 FILING DATE: 1998-04-24 APPLICATION NUMBER: 60/081818 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081817 FILING DATE: 1998-04-15

1998-04-24

APPLICATION NUMBER: 60/086414 FILING DATE: 1998-05-22 APPLICATION NUMBER: 60/086430

APPLICATION NUMBER: 60/087106 FILING DATE: 1998-05-28 FILING DATE: 1998-05-22

OR FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/08)
DR FILING DATE: 1998-06-10
DR FILING DATE: 19/98-06-11

APPLICATION NUMBER:

.998-06-10

60/088730

NUMBER: 60/088741 1998-06-10

60/088810

60/088858

FILING DATE: 1998-0 APPLICATION NUMBER: APPLICATION NUMBER:

1998-06-04

60/088026

APPLICATION NUMBER: 60/089532 FILING DATE: 1998-06-17

FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23

APPLICATION NUMBER: APPLICATION NUMBER: 60/ FILING DATE: 1998-06-17

60/089907 665680/09

APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-24

Score 1325;

В

9;

Length 243;

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CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
PULOT APPLICATION TEMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 362
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Saplen
US-10-123-904-362
                                                                                                                                           Query Match 100.0%; Score 1325; DB 9; Best Local Similarity 100.0%; Pred. No. 2.3e-89; Matches 243; Conservative 0; Mismatches 0;
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C54
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Matches 243; Conserv
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   APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYEAVHATVYRASLQFDLVKNGESIASFFQ 180
                                        MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
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Watanabe, Colin K
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Godowski, Paul J.
Gurney, Austin L.
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US-10-140-470-362
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APPLICANT: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K
Wood, William
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o. US20030022331A1
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; ORGANISM: Homo sapiens
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SEQ ID NO 68
LENGTH: 243
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OR APPLICATION NUMBER: 09/31
OR FILING DATE: 1999-05-14
OR APPLICATION NUMBER: 09/33
OR FILING DATE: 1999-06-18
OR APPLICATION NUMBER: 09/34
OR FILING DATE: 1999-06-29
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nes 243; Conservative
                                                  181 FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP 240
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FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP 240
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Gurney, Austin L.
Sherwood, Steven
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Filvaroff, Ellen
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0. US20030027270A1
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100.0%; Pred. No. 2.3e-89;
tive 0; Mismatches 0;
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Gaps

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RESULT 14
US-10-176-921-362
Sequence 362, Application US/10176921
Publication No. US20030027276A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-918-362
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Best Local Similarity
Matches 243; Conserv
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US-10-176-918-362
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LENGTH: 243
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C382
CURRENT APPLICATION NUMBER: US/10/176,918
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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Gurney, Austin L.
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5. US20030027275A1
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US-10-137-865-362
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Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550

SEQ ID NO 362
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-921-362
                                                                                                                                                                                                                              Sequence 362, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 1325; DB 9; Best Local Similarity 100.0%; Pred. No. 2.3e-89; Matches 243; Conservative 0; Mismatches 0;
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C288
CURRENT APPLICATION NUMBER: US/10/176,921
CURRENT FILING DATE: 2002-06-20
CURRENT FILING DATE: 2002-06-20
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Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin
                          Stewart, Timothy A
                                          Smith, Victoria
                                                            Sherwood, Steven
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o. US20030032155A1
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Godowski, Paul J.
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Filvaroff, Ellen
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Search completed: June 18, 2003, 15:02:35
Job time: 57 secs
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P333071C154
CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 362
LENCTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-10-137-865-362
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241 VFA 243
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Perfect score:
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243
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AAY93688
AAB01318
AAU12352
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AAB33461
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                                  NAB65815
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Human tumour-assoc
Human PRO344 prote
Human adipocyte-sp
Human PRO344 prote
Human PRO344 prote
Amino acid sequenc
Human PRO344 polyp
Human PRO344 polyp
Human TANGO 253 SE
Human adipocyte co
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AAY06481
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Human secreted pro	AAY02690	20	128	4.5	11	<b>4</b>
Human peptide enco		w	56	5	1	44
#3878	AAM05196	22	56	4.5	1	3
Peptide #4082 enco	2	22	56	4.5	1	42
#39	AAM17524	22	56	4.5	11	4
bone ma	AAM69711	22	56	4.5	11	40
rain ex	~	22	56	4.5	11	39
#3883	ABB21884	22	56	4.5	11	8
Peptide #4051 enco	ABB36545	22	56	4.5	11	37
#3990	ABB31339	22	56	4.5	11	36
s pep	242	22	27	4.5	11	35
Human TANGO 253 si	81	22	15	•	15	34
per	726	21	87	2	30	33
Murine TANGO 253 c	82	22	60		43	
TANGO 253	AAB65824	22	128		51	
TANGO 253	AAB65818	22	60	٠.	60	30
	AAB65899	22	243	5	62	29
secreted	AAB65898	22	243	5	62	28
secreted p	AAB65897	22	243	<u>ب</u>	62	27
TANGO 253	AAB65820	22	243	ū	62	26
	AAB65896	22	242	۶.	62	25
ine matur	AAB65821	22	228	5	62	24
ä	ABB72179	23	243	8	70	23
n cell pro	AAB55979	22	243	28.8	70	22
ξ.	AAY76040	21	243	8	70	21
human c	ABG12723	22	151	33.7	82	20
TANGO 25	AAB65819	22	128	2	128	19
secreted	AAB65890	22	243	8	142	18
secreted	AAB65889	22	243	٥.	148	17
secreted	AA021663	23	201		173	16
secreted	AAB65891	22	243		174	15
2	AAB65888	22	243	σ.	185	14
human d	272	22	220	7	213	13
mature TAN	658	22	228	93.8	228	12
Human adipocyte co	AAB49599	22	243	100.0	243	11

## ALIGNMENTS

20-NOV-1998; 05-JAN-1998; 29-APR-1998; Modified-site 05-JAN-1999; 15-JUL-1999 W09935170-A2 Protein Peptide Homo sapiens Modified-site 98US-0109304. 98US-0070440. 98US-0083500. 99WO-US00106 /note= "N-myristoylated" 216..243 /note= "mature protein"
68..215 /note= "signal peptide"
16..243 Location/Qualifiers /note= "N-myristoylated

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PRO344; UNQ303; cancer; tumour; diagnosis; therapy;

Human tumour-associated protein PRO344.

27-SEP-1999 AAY06481;

(first entry)

AAY06481 standard; Protein; 243 AA

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Query Match
Best Local S
Matches 243
                                                                                                                                                                                                                                                                                                                                               CC This sequence represents human PRO344 (UNQ303), a protein encoded CD by the novel cDNA clone DNA40592 (see AAX87258). Amplification of CDNA40592 was observed in primary lung tumours and in primary colon growth. Antagonists (e.g. antibodies) directed to PRO344 may have Last in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour cells. Such amplification is expected to be associated with overexpression of the gene product and to contribute to tumorigenesis. The encoded and/or treatment (including prevention) of certain cancers, and may each as predictors of the prognosis of tumour treatment. Antibodies that bind the proteins are claimed and used in claimed cancer.
Homo sapiens
               secreted protein;
                       Human; PRO protein;
                                         Human
                                                         12-AUG-1999
                                                                         AAY17827;
                                                                                         AAY17827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAY-1998;
10-JUN-1998;
10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 10; 162pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody against proteins expressed in neoplastic cells, useful tumor diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-430385/36.
N-PSDB; AAX87258.
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                                                                                                                                                                                  181
                                     PRO344 protein sequence
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                                                                                                                                                                                                                                                                                                  243;
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                                                                                                                                                                                                                                                          n 100.0%;
Similarity 100.0%;
43; Conservative (
                                                                                                                                                         standard;
                                                                                                                                                                                          VFA 243
                                                                                                                                               VFA 243
                                                                                                                                                                                                   APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
                                                                                                                                                                                                                                   APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                                                                                                                                           {\tt APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD}
                                                                                                                                                                                                                                                                                                                                 243 AA;
                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0086414.
98US-0088742.
98US-0107783.
         n; tumour necrosis factor family; TNF; cytokine; transmembrane protein; inflammation disorder.
                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gurney AL,
                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                            Score 243; DB 20;
Pred. No. 4.9e-212;
; Mlsmatches 0;
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The present invention describes nucleic acids encoding PRO secreted and transmembrane proteins used therapeutically. The PRO proteins have cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy, identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-371118/31.
N-PSDB; AAX80052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-1998;
03-DEC-1997;
11-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding PRO secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-DEC-1997;
16-DEC-1997;
17-DEC-1997;
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12-DEC-1997;
16-DEC-1997;
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                             241 VFA 243
                                                                                                                                                                                                                                                                                                                       Similarity
                                             MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
VFA 243
                                                                                                                                                                                       APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                                                                                     APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
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                                                                                                                                                                                                                                                                                                                                                                     243 AA;
                                                                                                                                                                                                                                                                                                     100.0%;
ilarity 100.0%;
Conservative 0
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97US-0069425
97US-0069696
97US-0069696
97US-0069870
97US-0069870
97US-0069873
97US-0068017
98US-0070440
98US-0070405
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                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                 Score 243; DB 20;
Pred. No. 4.9e-212;
                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and transmembrane
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                                                                                                                                                                                                                                                                                               Gaps
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AAW97984 standard; Protein; 243

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21-JUN-1999

(first entry)

Protein

/note= "signal peptide, alternatively
 peptide comprises residues 1...

the signal

"mature protein, alternatively the mature protein comprises residues 19..243

(specifically claimed

in Claim 4)"

0

Peptide

Location/Qualifiers

Homo sapiens

Adipocyte-specific protein; zsig39; human; energy balance; nutrition; antimicrobial. Human adipocyte-specific protein zsig39

fatty acid metabolism;

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Best Local S
Matches 243
                                                                                 haemostatic; antithyroid; antidabetic; nootropic; neuroprotective; antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic; antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarrhritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune thrombocytopaenia; immune-mediated renal disease; inflammatory bowel disease; hepatobiliary disease; whipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy;
                                                           autoimmune disease; immune-médiated skin disease; immunological disease; transplantation associated
                                                                                                                                                                                                                                                 Human;
                                                                                                                                                                                                                                                                                                                                                              AAB33461 standard; Protein;
                                                                                                                                                                                                                                  dermatological;
                                                                                                                                                                                                                                                                                                        29-JAN-2001
                                                                                                                                                                                                                                                                                                                                        AAB33461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               method of producing zsig39 polypeptide are claimed, as well as zsig39 polypeptides having N- or C-terminal affinity tags, toxins, radionucleotides, enzymes or fluorophores, fusion proteins including zsig39 polypeptides, an antibody that specifically binds to an epitope of zsig39, and a method for modulating free fatty acid metabolism by administering a zsig39 polypeptide. The zsig39 polypeptide may also be used in organ preservation, for zurgical pretreatment to prevent injury due to ischaemia and/or inflammation, and as an antimicrobial agent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acids and a cleavage site. A single EST sequence was discovered, and the novel polypeptide encoded by the full-length cDNA allowed the identification of a homologue relationship with adipocyte complement related protein Acrp30 and adipocyte secreted protein apM1. A full-length clone (see AAX24684) was obtained from tissue library. Expression vectors, cultured cells and a lung tissue library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                            241
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                                                     rejection;
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                                                                                                                                                                                                                                  immune related disease; diagnosis; antiinflammatory; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                            VFA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VFA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lysis or phagocytosis of infectious agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nilarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 AA;
                                                                                                                                                                                                                                                                         protein UNQ303
                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                               antiarthritic;
                                                                                                                                                                                                                                                                                                     entry)
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                                                                                                                                                                                                                  antirheumatic; immunosuppressive;
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Pred. No. 4.9e-212;
Mismatches 0;
                                                                                                                                                                                                                                                                       ID NO:241
                                                             allergic of disease;
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This polypeptide comprises human adipocyte-specific protein zsig39, a protein that modulates free fatty acid metabolism. zsig39 is a member of a family of proteins having a globular domain and a collagen-like domain capable of dimerisation or oilgomerisation. zsig39 polypeptides were initially identified by querying an EST database for secretory signal sequences characterised by an upstreament. upstream

esperanting the con-

Zsig39 protein - used to modulate fatty acid metabolism

111-112; 132pp; English.

(ZYMO ) ZYMOGENETICS

Sheppard PO

1999-204665/17. DB; AAX24684.

26-AUG-1997;

97US-0056983 98WO-US17724. Domain

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164..171

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note-

"beta "beta "beta

strand" strand\* strand\*

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/note-

"beta strand" "beta strand" "globular domain" "collagen-like domain"

"beta strand"

. . 139 . 146

/note-

. 243

note-105..109

28..130

/note-

. 23

note-

"beta strand "beta strand" "beta strand"

Doma in

/note= 170..17 111..135

174

"receptor binding domain" "receptor binding domain"

WO9910492-A1

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06-JAN-2000;
06-JAN-2000;
11-FEB-2000;
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20-DEC-1999;
30-DEC-1999;
05-JAN-2000;
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13-SEP-1999;
15-SEP-1999;
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28-JUL-1999;
01-SEP-1999;
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29-NOV-1999;
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23-JUN-1999;
20-JUL-1999;
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04-MAY-1999;
14-MAY-1999;
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12-APR-1999;
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10-MAR-1999;
12-MAR-1999;
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2000WO-US00219.
2000WO-US00277.
2000WO-US00376.
2000WO-US03565.
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2000WO-US04414
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99US-0144758.
99US-0145698.
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99US-0131445.
99US-0132371.
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99WO-US28565
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99WO-US28313
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## (GETH ) GENENTECH INC.

Ashkenazi AJ, Kabakoff RC, ŢĄ, ر ر Tumas D, Baker KP, Lu Y, Pan Pan J, P, Goddard A, Gurney AL, Heb an J, Pennica D, Shelton DL, Watanabe CK, Wood WI, Yan M; Goddard A, Hebert C, DL, Smith **Henzel** 

2000-572271/53. DB; AAC58626.

Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumato arthritis, osteoarthritis, thyroiditis and diabetes mellitus. rheumatoid

Fig 96; 309pp; English.

The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's systemic systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory disease, gluten-sensitive enteropathy and whipple's disease, mmune or immune-mediated skin diseases, allergic diseases,

01-DEC-1998;

98WO-US25108

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RESULT 5
AAY71468
ID AAY7
AC AAY7
XX AAY7
XX DT 08-1
XX PRO
KW PRO
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                                          30-NOV-1999;
                                                                                        08-JUN-2000
                                                                                                                                                                                                Modified-site
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                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRO344;
                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PRO344 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neoplastic cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY71468 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AAC58397 to AAC58578 represent PCR primers and hybridisation probes in the isolation of human PRO sequences. AAC58599 to AAC58642 and AAB33414 to AAB33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; DNA40592-1242; human; ATCC No: 209492; antiproliferative; lastic cell growth inhibitor; cytostatic; treatment; cancer; tumour; st; prostate; colon; lung; renal; ovarian; central nervous system; leukemia; melanoma; Expressed Sequence Tag; EST; secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VFA 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain;
                                        99WO-US28409
                                                                                                                                                                                                   /note=
216..2
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                                                                                                                                                                                                                                                /note= "N-myristoylation site"
77..80
                                                                                                                                                                                                                                                                                                                                                                                   /label= Signal_peptide
11..17
                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                              'label=
                                                                                                                                                                                                                                                                                                                                                    'note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
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                                                                                                                                                                                                                 "Cell attachment sequence"
                                                                                                                                                                      "N-myristoylation site"
                                                                                                                                                                                                                                                                                                       Mature_PRO344_protein
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Pred. No. 4.9e-212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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RESULT 6
AAY93688
ID AAY9
XX AAY9
XX O3-C
XX O3-C
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XX PRO;
KW PRO;
KW PRO;
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Best Local S
Matches 243
                                               PRO201;
PRO715;
                    Homo sapiens.
                                      tumourigenesis;
                                                                          Amino acid
                                                                                                                             AAY93688 standard;
                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the human PRO344 protein, encoded by the cDNA clone, designated as DNA40592-1242. It is isolated from human foetal lung tissue, cDNA library, identified using probes based on a consensus sequence DNA34398, derived from secreted protein extracellular domain NC (ECD) expressed sequence tag (EST). This clone is assigned ATCC deposit NC: 209492. PRO344 functions as a neoplastic cell growth inhibitor and is used for treating tumours, using an effective amount of PRO555, PRO364 and PRO344. This composition is especially useful for treatment of human cancers such as breast, prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-DEC-1998;
22-DEC-1998;
20-JUL-1999;
26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                composition useful for inhibiting neoplastic cell
ating cancers, comprises PRO655, PRO344 or PRO364 p
ir antagonists -
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                                                                                                                                                                                                                                                                                                                                                           1 Similarity
243; Conserv
                                            PRO292; PRO327; PRO1265; PRO1017; PRO1112; PRO509;
                                                                                                                                                                                                                                                                                                                       -
                                                                                                                                                                                                                  FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
                                                                                                                                                                                                                                           VFA 243
                                                                                                                                                                                                        FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
                                                                                                                                                                                                                                                                                                                          MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGRDGAPG
                                                                                                                                                                           VFA 243
                                                                                                                                                                                                                                                                               APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                                                                                                                                                                                                         APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVDPRSAFSAKRSESRVDPPSD
                                                                                                                                                                                                                                                                                                                  MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goddard A,
                                                                     sequence of novel polypeptide PRO344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Flg 6;
                                                                                                                                                                                                                                                                                                                                                                                             243 AA;
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                        (first entry)
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98US-0113296:
99US-0144758.
99US-0145698.
                                     cancer;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108pp; English.
                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                     neoplastic
                                                                                                                              243
                                                                                                                                                                                                                                                                                                                                                         0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL,
                                                                                                                                                                                                                                                                                                                                                               Score 243; DB 21;
Pred. No. 4.9e-212;
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                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                          PRO344; PRO343; PRO347; PRO357; PRO853; PRO882; tumour cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillan K,
                                     cell
                                    growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Napier M,
                                                                                                                                                                                                                                                                                                                                                       0;
                                 cell proliferation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l growth and polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wood
                                                                                                                                                                                                                                                                                                                                                                        243;
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                                                                                                                                                   Matches
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Best Local
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01-DEC-1999;
02-DEC-1999;
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08-MAR-1999;
02-JUN-1999;
01-SEP-1999;
15-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                              Botstein Wood WI;
                                                                                                                                                                                     Sequence
                                                                                                                                                                                                     and proliferation
                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUN-2000
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                      181
                                        121
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DB; AAA46907.
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                                                                                                                                                  al Similarity
243; Conserv
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                                                                                                                                                                                     243 AA;
                                                                                                                                                                                                                                                                                                                                                                                      Goddard
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/note=
11..17
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The present sequence represents a novel human polypeptide. The specification describes novel polypeptides designated PRO201, PRO292, PRO327, PRO1265, PRO344, PRO347, PRO357, PRO715, PRO1017, PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumourigenesis. The polypeptides are useful target for the identification of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies against these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 61; Fig 10; 220pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New anti-polypeptide antibody useful in the treatment and neoplastic cell growth and proliferation - \,
APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
                                                                                                                                                             APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                                                                                                                                                 MRPLLVLLLIGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
                                                                    APLPEDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
                                                                                                                                          APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                                                                                                                                MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
                                                                                                                                                                                                                                                                                          Conservative
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99WO-US12252.
99WO-US20111.
99WO-US21090.
99WO-US28313.
99WO-US28409.
99WO-US28301.
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216..22
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68..74
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77..80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "N-myristoylation
                                                                                                                                                                                                                                                                                                     0.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gurney
                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                     Score 243; DB 21;
Pred. No. 4.9e-212;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL,
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RESULT 7

AABO1318

ID AABO
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KW PRO3
KW PRO3
KW ANTI
OS HOMO
XX PRO4
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FT MOd1
FT MOd1
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FT POL9
FT POL9
RN WO20
XX WO20
PR 01-D
XX PF 01-D
XX COL1
CC New
CC POL9
CC Incl
CC Small
CC Anti
CC Anti
CC Anti
      Query Match
Best Local Similarity
Matches 243; Conser
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                                                                New human nucleic acids encoding secreted and transmembrane polypeptides which are designated as PRO polypeptides are described. The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources.
                                                                                                                                                                                                                                                                                                                                     01-DEC-1998;
16-DEC-1998;
22-DEC-1998;
                                                                                                                                                                                         New human nucleic acids of polypeptides, designated and diagnostic agents
                                                  Sequence
                                                                                                                                                                  Claim 12; Fig 18; 187pp; English.
                                                                                                                                                                                                                                      WPI; 2000-412324/35.
N-PSDB; AAA49560.
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Gerritsen ME, Goddard A,
Hillan KJ, Kljavin IJ, /
                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
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        Conservative
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98US-0112850.
98US-0113296.
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68.74
/note= "N-myristoylation site"
77.80
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Cell attachment sequence 216..222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Signal peptide
11..17
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1..15
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                 100.0%;
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                                                                                                                                                                                               encoding secreted and transmembrane
d as PRO polypeptides, useful as pharmaceutical
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A, Godowski PJ, Grimaldi CJ, Gurn
Napier MA, Roy MA, Tumas D, Woo
      0;
    Score 243; DB 21;
Pred. No. 4.9e-212;
Mismatches 0;
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                        Length
    Indels
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RESULT 8
AAU12352
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21-MAR 2000
30-MAR 2000
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30-MAY 2000
30-MAY 2000
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02-DEC-1999;
09-DEC-1999;
16-DEC-1999;
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01-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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breast; prostate; cervical; tur
cartilage; ear; proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secretory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO344 polypeptide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRPLLVLLLIGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
99WO-US30999
99WO-US30299
2000WO-US00277
2000WO-US00376
2000WO-US04341
2000WO-US04414
2000WO-US04414
2000WO-US04414
2000WO-US04914
2000WO-US05601
2000WO-US05601
2000WO-US07377
2000WO-US014705
2000WO-US014705
2000WO-US14705
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2000WO-US14705
2000WO-US14705
2000WO-US14705
2000WO-US13705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A-peptide; factor VIIA; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                           2000WO-US32678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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99WO-US28565.
99US-0170262.
99WO-US30095.
99WO-US30911.
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99WO-US28551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mbrane; PRO; mammalian; cancer; lung;
tumour necrosis factor-alpha; TNF-alpha;
on; glucose; free fatty acid; skeletal mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 AA
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RESULT 9
AAB65815
ID AAB6
XX
AC AAB6
XX
DT 28-M
XX
DE Huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing CC PRO polypeptides, and to detect the presence of mammalian lung, colon, CC breast, prostate, rectal, cervical or liver tumours by comparing PRO CC Some of the 275 sequences are also useful to stimulate the release of proliferation or differentiation of chodrocytes, the proliferation or certilage, the proliferation of inner ear utricular supporting cells or T. lymphocytes, the release of a cytokine from peripheral blood CC monocytes, the proliferation of inner ear utricular supporting cells or CC monocytes, the proliferation of a cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify CC molecules involved in binding interactions. The polypucleotides encoding transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 243
                          28-MAR-2001 (first entry)
                                                                                   AAB65815 standard;
Human TANGO 253 SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU12172-AAU12446 r
PRO polypeptides. T
PRO polypeptides, t
PRO polypeptides, t
PRO polypeptides, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Gerritsen ME, Goddar
Smith V, Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                        APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
                                                                                                                                                                                                                                                                                                                                MRPLLVLLLGGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGRDGAPG
                                                                                                                                                                                                                                                                                      APLPFDRVLVNEOGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
                                                                                                                                                                                                                                                                                                                                                                                         MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 AA;
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ME, Goddard
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        represent novel human secretory and transmembrane The PRO polypeptides are useful to detect other to link bloactive molecules to cells expressing to modulate biological activities of cells expressing
                                                                                     Protein;
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.0%;
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Pred. No. 4.9e-212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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Human; zacrp5; gene therapy; complement inhibition;

Clq domain;

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RESULT 10
AAB49593
WXX DXX AXX
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Matches
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                Human adipocyte complement related protein homolog zsig39.
                                                   13-MAR-2001
                                                                                                        AAB49593 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human and murine secreted or transmembrane proteins TANGO 253, TANGO 25 TANGO 281 and INTERCEPT 258. These are useful in the treatment of coronary, pulmonary, olfactory, immunological, neurological, developmental and kidney disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acids for treating diseases and disorders, e.g. atherosclerosis, infection, autoimmune diseases, obesity, ear disorders, brain disorders, tumors, diabetes, arthritis, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leiby KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281; INTERCEPT 258; coronary disorder; olfactory disorder; neurological disorder; pulmonary disorder; immunological disorderevelopmental disorder; kidney disorder.
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                                                                                                                                                                                                                                                                                                                                       APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                                                                                           VFA 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McKay C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 AA;
                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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Pred. No. 4.9e-212;
; Mismatches 0;
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The present invention relates to human adipocyte complement related protein homolog, zacrp5 protein and coding sequence (see AAB49590 and AAC90045). ZACRP5 has a carboxyl-terminal Clq domain. The zacrp5 gene is Cloated on human chromosome 16 zacrp5 gene and protein are useful for creation, but the constant of carboxyl-terminal Clq domain. The zacrp5 gene is Claimosing and treating inflammations, for determining arterial cremodelling, for modulating calcium ion concentration, hormone cremodelling, for calcium ion concentration, pastric emptying, human carbitonate release, phospholipase c activation, gastric emptying, human carried generally against bacteria and virus, for complement inhibition, for creating acute vascular injury, and for wound healing. The present creating acute vascular injury, and for wound healing. The present sprotein. This protein was used in a sequence homology alignment with
                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infections, and in wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel adipocyte complement related protein homolog, ZACRP5, useful for diagnosing and treating inflammation, vascular injury microbial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-061531/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adipocyte complement related protein homolog; inflammation; hormone secretion; inositol phosphate; arachidonate; phospholipase C activation; gastric emptying; neutrophil activation; superoxide anion production; antimicrobial; acute vascular injury; wound healing; zsig39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (2YMO ) ZYMOGENETICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens.
                                            MRPLLVLLLIGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGRDGAPG
                                                                                                                                                                                                                                                                                                                         Similarity
VFA 243
                             VFA 243
                                                                                                                                                                                    APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                                                                                    APGEKGEGGRPGLPGPRGDPGPRGEAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                                                                                                                                                                                                                                                                                       243 AA;
                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                 Score 243; DB 22;
Pred. No. 4.9e-212;
                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                sequence homology alignment with
                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                243;
                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                             Gaps
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AAB49599

RESULT 11

Дb Q DЬ ρ . <del>В</del>

121 121 61 61

FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP

240 180 180 120 120

APLPEDRVĹVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESJASFFQ APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ

APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGDAGECSVPPRSAFSAKRSESRVPPPSD Matches

Similarity

100.08; ilarity 100.08; Conservative C

0

Score 243; DB 22; Pred. No. 4.9e-212; Mismatches 0;

Length Indels

243; 0

Gaps

0

60 60

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The Present Anyenchom treaters to imment analyticy to complement related 2C ARC99051). ZACRP6 protein and coding sequence (see AAB49596 and 2C located on human chromosome 21q. zacrp6 gene and protein are useful for 2C diagnosting and treating inflammations, for determining arterial for 2C remodelling, for modulating calcium ion concentration, hormone 2C carachidonate release, phospholipase C activation, gastric emptying, human 2C carcef gene and protein are useful for 2C neutrophil activation or ADCC capability and superoxide anion production. 2C carcefing against bacteria and virus, for complement inhibition, for 2C treating acute vascular injury, disseminated intravascular coagulation, 2C cadipocyte complement related protein homolog zsig39. This protein was 2c used in a sequence homology comparison with ZACRP6 protein was 2c used in a sequence homology comparison with ZACRP6 protein was 2c used in a sequence homology comparison with ZACRP6 protein
Query Match
Best Local :
                                                    Sequence
                                                                                                                                                                                                                                                                                                                              The present invention
                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   Novel adipocyte complement related protein homolog, ZACRP6, useful as modulators of neurotransmission and for treating disseminated intravascular coagulation, arteriosclerosis and acute vascular injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-061532/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piddington CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAY-2000; 2000WO-US14024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; zacrp6; gene therapy; complement inhibition; Clq domain; adipocyte complement related protein homolog; inflammation; hormone secretion; inositol phosphate; arachidonate; phospholipase C activation; gastric emptying; neutrophil activation; superoxide anion production; antimicrobial; acute vascular injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W0200073446-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human adipocyte complement related protein homolog zsig39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                wound healing; zsig39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB49599 standard; Protein;
                                                  243
                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9908-0321262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sheppard
                                                                                                                                                                                                                                                                                                                 relates to human adipocyte complement related
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                                                                                                                                                                           production.
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RESULT 12
AAB65816
ID AAB658
AC AAB65
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Best Local s
Matches 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of human and murine secreted or transmembrane proteins TANGO 253, TANGO 281 and INTERCEPT 258. These are useful in the treatment of coronary, pulmonary, olfactory, immunological, neurological, developmental and kidney disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acids for treating diseases and disorders, e.g. atheroscierosis, infection, autoimmune diseases, obesity, ear disorders, brain disorders, tumors, diabetes, arthritis, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 212-213; 332pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-050109/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leiby KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUN-2000; 2000WO-US16883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W0200078808-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281; INTERCEPT 258; coronary disorder; olfactory disorder; neurological disorder; pulmonary disorder; immunological disorder; kidney disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human mature TANGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB65816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB65816 standard; Protein; 228 AA
                                   181
                                                                                                                         136 YDAYTGKFTCQYPGYYYFAYHATYYRASLQFDLYKNGESIASFFQFFGGWPKPASLSGGA 195
                                                                                                                                                                                                                                                                                                                                                                                                             228;
                                                                                                                                                                                             61 PRODPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLDFDRVLVNEQGH
                                                                                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
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       SPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                YDAVTGKETCQVPGVYYFAVHATVYRASLQEDLVKNGESIASEFQEFGGWPKPASLSGGA
                                                                                                                                                                                                                       PRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGH 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McKay C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VFA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VFA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                            93.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 228; DB 22;
Pred. No. 1.8e-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                               1.8e-198;
                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 228;
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                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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GO 257,
                                                                                                     180
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CC polymerase chain reaction (PCR) primers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC are to restore normal activity of (II) is useful in gene therapy techniques (CI). (II) is useful for generating antibodies against it, detecting or CC a food supplement. (II) and its binding partners are useful in medical collarating of sites expressing (II). (I) and (II) are useful for treating or CC imaging of sites expressing (II). (I) and (II) are useful for treating classorders involving aberrant protein expression or biological activity. CC diagnostics, forensics, gene mapping, identification of mutations in cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human cc specification, but was obtained in electronic format directly from wIPO cat first two solutions of the invention.
                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID No 43083; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity .
                                                                                                                                                                                                                                                                                                                                                    The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-639362/73.
N-PSDB; AAS76911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #12715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG12724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG12724 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cood supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
                                                                                                                                                                                                                                                                                                                  relates to isolated polynucleotide (I) and II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; gene mapping; gene therapy; forensic
imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TY
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Matches
                             Query Match
                   Loca
     h 87.7%; Sc
Similarity 100.0%; P
13; Conservative 0;
             Score 213; DB 22;
; Pred. No. 6.9e-185;
     Mismatches
    0,
                       Length 220;
  Indels
  0,
Gaps
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Sequence

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EAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFT

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AAB65888
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                                                                                                                                                                    Sequence
                                                                                                                                                                            The present invention provides the protein and coding sequences of the human and murine secreted or transmembrane proteins TANGO 253, TANGO 257, TANGO 281 and INTERCEPT 258. These are useful in the treatment of coronary, pulmonary, olfactory, immunological, neurological, developmental and kidney disorders.
                                                                                                                                                                                                                                                             New nucleic acids for treating diseases and disorders, e.g. atherosclerosis, infection, autoimmune diseases, obesity, ear disorders, brain disorders, tumors, diabetes, arthritis, multiple sclerosis and asthma
                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                    WPI; 2001-050109/06
                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                              18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                              19-JUN-2000; 2000WO-US16883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281; INTERCEPT 258; coronary disorder; olfactory disorder; neurological disorder; pulmonary disorder; immunological disorder; developmental disorder; kidney disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                     28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200078808-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB65888 standard; Protein;
            179
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                                                                                                                              185;
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                                                                                                                                      Similarity
           FOFFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGELVYSDWHS
                                       SDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASF
                                                 SDAPLPFDRVLVNEOGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQEDLVKNGESIASF
                                                                            61
FQFFGGWPKPASLSGGAMYRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHS
                                                                                                                                                                   243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McKay C,
                                                                                                                          76.1%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                          Page 270-271; 332pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                            9908-0336536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein related
                                                                                                                                                                                                                                                                                                                                     Bossone S;
                                                                                                                           0;
                                                                                                                    Score 185; DB 22; I
Pred. No. 1.8e-159;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein SEQ ID NO: 102.
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                                                                                                                                         Length 243;
                                                                                                                      Indels
                                                           178
                                       178
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RESULT 15
AAB65891
XX AAB65
XX AAB65
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XX Human
XX Human
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PN WO200
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences of the human and murine secreted or transmembrane proteins TANGO 253, TANGO 257, TANGO 281 and INTERCEPT 258. These are useful in the treatment of coronary, pulmonary, olfactory, immunological, neurological, developmental and kidney disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acids for treating diseases and disorders, e.g. atherosclerosis, infection, autoimmune diseases, obesity, ear disorders, brain disorders, tumors, diabetes, arthritis, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-050109/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leiby KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUN-2000; 2000WO-US16883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281; INTERCEPT 258; coronary disorder; olfactory disorder; neurological disorder; pulmonary disorder; immunological disorder; developmental disorder; kidney disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-1999;
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                       121
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                                                                                                                     61
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                                                                                                                                                                                                                       1 MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
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                                                                                                                                                                                                                                                                                                                                       Similarity
APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGES
                          APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGES
                                                                                               APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                                          APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                                                                                                               MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 274; 332pp; English
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; Pred. No. 1.7e-149;
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Search completed: June Job time: 77 secs

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AND CONTRACTOR

10 4.1 702 2 C97884 110 4.1 102 2 S31521 10 4.1 1464 2 S59856 10 4.1 1464 2 S59856 10 4.1 1466 1 CGHU7L 10 4.1 2551 2 B9847 9 3.7 126 2 S53786 9 3.7 246 2 S38344 9 3.7 356 2 S16907	4.5 369 2 \$33603 4.5 374 1 A42046 4.5 374 1 A42046 4.5 374 1 CGHU3B 4.5 1670 1 CGHU3B 4.5 2944 2 A54849 4.1 210 2 B44984 4.1 248 1 LUNGPS 4.1 248 2 A48853 4.1 248 2 A48853 4.1 248 2 A48853 4.1 447 2 T42987 4.1 694 2 B45046	Score Match Length DB ID 219 90.1 219 2 T14782	Pred. No. is the number of results predicted by chance score greater than or equal to the score of the result and is derived by analysis of the total score distribution.  SUMMARIES	Database: PIR_73:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*	Total number of hits satisfying chosen parameters: 283224 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Listing first 45 summaries	size: 0	seqs, 96134422 r	ble:	Title: US-09-943-851A-42 Perfect score: 243 Sequence: 1 MRPHIVITIGE ACCEPTED	Run on: June 18, 2003, 15:01:43; Search time 40 seconds (without alignments) 584.017 Million cell updates	OM protein - protein search, using sw model	GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
hypothetical prote hypothetical prote collagen COLF1 - f collagen alpha 1(I C;Species: Caenorhabditis elegans collagen alpha 1(I C;Species: Caenorhabditis elegans collagen alpha 1(I C;Species: Caenorhabditis elegans collagen alpha 1(I C;Cate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000 collagen type IV a hypothetical prote collagen alpha 1(I C;Cate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000 C;Cate: 29-Oct-1999 #sequence_revision 29-Oct	hypothetical prote surfactant protein pulmonary surfacta Db 121 CovpGvyYFAVHATVYRASLOFDLVKNGESIASFFQFFGGMPKPASLSGGAMVRLEPEDQ 18 pulmonary surfacta	Query Mat Best Loca Matches	A;Cross-refe A;Experiment C;Genetics: A;Note: DKFZ C;Superfamil	submitted to the Protein Sequence Database, August 1999 A. Reference number: 218184 A. Accession: T14782 A. Status: preliminary A. Molecule type: mRNA A. Residue: 1-210 (2007)	RESULT 1  T14/82  hypothetical protein DKFZp586B0621.1 - human (fragment) C. Species: Homo sapiens (man) C. Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_cha C. Accession: T14/82 R. Ottenwalder B. Obermain	ALIGNMENTS	CAP18 precurse	243 42 8 3.3 149 2 B81002 43 8 3.3 164 2 \$76920 44 8 3.3 170 2 \$74248 45 8 3.3 170 2 \$74248	. 41 8 3.3 149 2	36 9 3.7 1752 2 A45407 collagen all 37 9 3.7 2288 2 729999 hypothetical 38 8 3.3 46 2 165268 collagen all	9 3.7 964 1 CGC1800 9 3.7 1402 2 146707	9 3.7 636 2 S41067 9 3.7 751 2 A49974 9 3.7 765 2 S42800

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QY 205 VWVQVGVGDYIGIYASIKTDSTESGFLVYSDWHSSPVFA 243	OY 145 COVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWFKPASLSGGAMVRLEPEDQ 204	61	25	Query Match 90.1%; Score 219; DB 2; Length 219; Best Local Similarity 100.0%; Pred. No. 1.5e-199; Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps	A;Note: DKFZp586B0621.1 C;Superfamily: complement Clq carboxyl-terminal homology	A;Cross-references: EMBL:AL110261 A;Experimental source: adult uterus; clone DKFZp586B0621 C;Genetics:	A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-219 <pre>A; Resid</pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre>	Submitted to the Protein Sequence Database, August 1999 A;Reference number: 218184 A;Accession: T14782	hypothetical protein DKFZp586B0621.1 - human (fragment) C:Species: Homo sapiens (man) C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Sep-2000 C:Accession: T14782	RESULT 1
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                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <SHI>
                                                                                                                                                                                                                                                           R:Shimizu, H.; Fisher, J.H.; Papst, P.; Benson, B.; Lau, K.; Mason, R.J.; Voelker, D.R. J. Biol. Chem. 267, 1853-1857, 1992

A;Title: Primary structure of rat pulmonary surfactant protein D. cDNA and deduced aming A;Reference number: A42046; MUID:92112913; PMID:1370483

A;Accession: A42046
                                                                                                                                                                                                                                                                                                                                        surfactant protein D - rat
C;Speckes: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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Immunology 78, 159-165, 1993
A:Title: Structural similarity between bovine conglutinin and A:Reference number: S33603; MUID:93170856; PMID:8436402
A;Accession: S33603
                                                                                                                                                                                                                                                                                                                          R;Shimizu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       surfactant protein D - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
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A;Experimental source: strain Bristol N2; clone F26F12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-289 <WIL>
                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: pulmonary surfactant protein D; C-type lectin homology (248-367/Domain: C-type lectin homology <LCH>
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0.02;
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0.016;
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A;Residues: 202-257 <HOFF
A;Residues: 202-257 <HOFF
A;Rust, K.; Grosso, L.; Zhang, V.; Chang, D.; Persson, A., A., A., A., Arch. Biochem. Biophys. 290, 116-126, 1991
A;71tle: Human surfactant protein D: SP-D contains a C-type lectin carbohydrate recognication of the protein by the protein B 1898081
                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: sequence extracted from NCBI backbone (NCBIP:123024, NCBIP:123023); sequence C;Comment: Pulmonary surfactant is a complex of phospholipids and proteins that lower C;Comment: This protein is synthesized by alveolar type II cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 46-58,'F',60-62,'E',64-72;223-227,'X',229-239,'P',241-245,'X',247-256,'X'
A;Cross-references: PIDN:AAB25037.1; PID:9263973; PIDN:AAB25038.1; PID:9263974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Crouch, E; Persson, A.; Chang, D. Am. J. Pathol. 142, 241-248, 1993
Am. J. Title: Accumulation of surfactant protein D in human pulmonary alveolar proteinosis A;Reference number: A56776; MUID:93142849; PMID:8424457
A;Accession: A56776
                                                                                                                                                                                                                                                                                                A;Cross-references: GDB:132674; OMIM:178635
A;Map position: 10q22.2-10q23.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: bronchoalveolar lavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 'F',60-205,'P',207-374,'HF' <RUS>
A;Cross-references: GB:L05485; NID:9292505
                                                                                                                                                                                                                                                                                                                                                                     A; Gene: GDB:SFTPD; SFTP4; SP-D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Molecule type: protein
A; Residues: 214-234, 'x', 236, 'xx', 239-241 <LUJ2>
R; Hoppe, H.J.; Barlow, P.N.; Reid, K.B.M.
FEBS Lett. 344, 191-195, 1994
                                                                               Superfamily: pulmonary surfactant protein D; C-type lectin homology; Keywords: blocked amino end; calcium; glycoprotein; hydroxylysine; hyd; 1-20/Domain: signal sequence #status predicted <SIG>1-1-375/product: pulmonary surfactant protein D #status predicted <MAT>1-1-5/Domain: non-collagenous #status predicted <NCI>1-1-5/Domain: collagenous #status predicted <NCI>1-6-222/Domain: collagenous #status predicted <COL
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R;Lu, J; Willis, A.C.; Kelu, N.C...
Biochem. J. 284, 795-802, 1992
A;Title: Purification, characterization and cDNA cloning of human
Note: Purification, characterization and cDNA cloning of human
Note: Purification, characterization and cDNA cloning of human
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A; Residues: 202-257 < HOP>
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A;Residues: 1-30,'T', 32-121,'P',123-179,'A',181-375 <LUJ1>
A;Cross-references: EMBL:X65018; NID:g34766; PIDN:CAA46152.1;
A;Experimental source: lung
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C;Date: 16-Apr-1999 #sequence_revision 16-Apr-1999 #text_change 22-Jun-1999
C;Accession: A4525; S24434; S2455; S44420; S18382; A56776
R;Crouch, E; Rust, K; Veile, R; Donis-Keller, H; Grosso, L.
J. Biol. Chem. 268, 2976-2983, 1993
A;Title: Genomic organization of human surfactant protein D (SP-D). SP-D is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
**Postdues: 1-375 <CRO>
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A;Reference number: A45225; MUID:93155122; PMID:8428971
                               223-375/Domain: non-collagenous #status predicted 254-373/Domain: C-type lectin homology <LCH>
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A;Contents: annotation; erratum; correction to intronic sequence in A44043 R; Bernal, D.; Quinones, S.; Saus, J.
J. Biol. Chem. 268, 12090-12094, 1993
A;Title: The human mRNA encoding the Goodpasture antigen is alternatively s A;Reference number: A45971; MUID:93280184; pMID:8505332
A;Accession: A45971
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1427-1444 <BEP>
A;Note: sequence extracted from NCBI backbone (NCBIP:133363); sequence inco Am. J. Hum. Genet. 49, 545-554, 1991
A;Title: Sequence and localization of a partial cDNA encoding the human alp A;Accession: A39786; MUID:91353570; pMID:1882840
A;Molecule type: mRNA
A;Reference number: A39786; MUID:91353570; pMID:1882840
                                                                                                 A; Molecule type: mRNA
A; Residues: 1453-1593, 'A', 1595-1670 <MOR>
A; Residues: 1453-1593, 'A', 1595-1670 <MOR>
A; Cross-references: GB: 555790; NID: 9234418; PIDN: AAB19637.1;
C; Comment: Prolines and lysines at the third position of the ed and subsequently O-glycosylated.
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A;Note: sequence extracted from NCBI backbone (NCBID:11597)
R;Quinones, S.; Bernal, D.; Garcia-Sogo, M.; Elena, S.F.; Saus, J.
J. Biol. Chem. 269, 17358, 1994
A;Reference number: A44738; MUID:94274734; PMID:8006044
A;Contents: annotation; erratum; correction to intronic sequence in A4404
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C;Date: 28-Oct-1994 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999
C;Accession: A54763; A43928; A44043; A4591; A39786
R;Mariyama, M.; Leinonen, A.; Mochizuki, T.; Tryggvason, K.; Reeders, S.T.
J. Biol. Chem. 269, 23013-23017, 1994
A;Title: Complete primary structure of the human alpha3(IV) collagen chain.
A;Reference number: A54763; MUID:94364994; PMID:8083201
N;Cross-references: GDB:128351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A44043
A; Molecule type: DNA;
A; Residues: 1386-1670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-1670 <MAR>
A;Residues: 1-1670 <MAR>
A;Cross-references: GB.X80031; NID:9577563; PID:9577564
A;Experimental source: kidney
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A;Title: Molecular cloning of the human Goodpasture antigen demonstrates it to be A;Reference number: A43928; MUID:92147878; PMID:1737849
A;Accession: A43928
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i;Residues: 1331-1524,'I',1526-1670 <TUR>
h;Cross-references: GB:MB1379
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9784, 1992
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     A; Cross-references:
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C;Species: Homo sapiens (man)
C;Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change
C;Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change
C;Accession: A54849; PH0844; S16316; I56328; A30296; I84686
R;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J.
J. Biol. Chem. 269, 20256-20262, 1994
A;Title: Cloning of human type VII collagen. Complete primary se
A;Reference number: A54849; MUID:94327588; PMID:8051117
A;Accession: A54849
                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 815-892, 'E', 894-1439 <PAR>
                                                                                                                                                                                                                                                                                   R;Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A;Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the A;Reference number: S16316; MUID:91334380; PMID:1871109
                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 'EFR', 340-475, 'RALSTASHSTICWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG', 524-528,'
A;Cross-references: DDBJ:D11152; DDBJ:D13694; NID:9453698; PIDN:BAA02853.1; PID:94536
A;Experimental source: keratinocyte
A;Experimental source: keratinocyte
A;Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
A;Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
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A; Residues: 1-2944 <CHR>
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(Keywords: alternative splicing; basement membrane; cell b
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-1670/Product: collagen alpha 3(IV) chain, long splice
F:29-42/Domain: amino-terminal nonhelical, NH1 <NH1>
F:49-1438/Region: interrupted helical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Map position: 2936-2937
A:Introns: 1385/1; 1418/1; 1488/1; 1547/2; 1585/3; 1643/2 #status incomplete A:Introns: 1385/1; 1418/1; 1488/1; 1547/2; 1585/3; 1643/2 #status incomplete strange of the alpha 3(IV) and alpha 4(IV) chain genes are encoded on opposite strange; C:Complex: This minor type IV collagen is thought to form a heterotrimer of two among trimer amino-terminal domains (with disulfide and desmosine cross-links), der associations in the interrupted helical domain (with disulfide and desmosine companies).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;791-793/Region: cell attachment (R-G-D) motif
F;996-998/Region: cell attachment (R-G-D) motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Description: minor structural component of extracellular basement membrane in kidne C; Superfamily: collagen alpha 1(IV) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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    Complete primary sequence of the alphal(
PMID:8051117

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0.074;
                                                                                                                                                                                                                                                                                                                                                                               for residues 394 and Woodley, D.T.; Wynn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
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Section A in
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GB:M65158; keratinocyte

GB:S49017; NID:g180914; PIDN:AAA96439.1;

PID:g180915

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E;954-1045/Dommain: ....

F;1052-1219/Dommain: von Willebrand factor type notif
F;11052-1219/Dommain: von Willebrand factor type notif
F;1170-1172/Region: cell attachment (R-G-D) motif
F;1189-1253/Region: cysteine/proline-rich
F;1254-2783/Region: interrupted helical
F;1334-1336/Region: cell attachment (R-G-D) motif
F;2008-2010/Region: cell attachment (R-G-D) motif
F;2553-2555/Region: cell attachment (R-G-D) motif
F;2653-2555/Region: cell attachment (R-G-D) motif
F;2653-2555/Region: carboxyl-terminal nonhelical *status predicted cyste;2640/Dommain: carboxyl-terminal nonhelical *status predicted cyste;2640/Dommain: carboxyl-terminal nonhelical *status predicted cyste;2651/Modified site: carbohydrate (Asn) (covalent) *status predicted cyste;2651/Modified site: 5-hydroxylysine (Lys) *status experimental cyste;2625,2631/Binding site: carbohydrate (Lys) (covalent) *status experimental cyste;2625,2631/Binding site: carbohydrate (Lys) (covalent) *status experimental cyste;2625,2631/Binding site: carbohydrate (Lys) *status experimental cyste;2625,2631/Binding
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A;Cross-references: GDB:128750; OMIM:120120
A;Map position: 3p21.3-3p21.3
A;Note: defects in this gene can result in dominant and recessive
A;Note: there are 118 introns
C;Complex: type VII collagen is probably a homotrimer
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A; Residues: 2395-2871, 'S', 2873-2944 <RE2>
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A;MoLecule type: mRNA
A;Residues: (ERK, 372-517, DV', 520-540, 'W', 542-1255 <RES>
A;Cross-references: GB:S51236; NID:g262308; PIDN:AAB24637.1; PID:g262309
R;Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.;
J. Blol. Chem. 264, 3822-3826, 1989
A;Title: Cleavage of type VII collagen by interstitial collagenase and type A;Reference number: A30296; MUID:89139437; PMID:2537292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hum. Mol. Genet. 2, 273–278, 1993
A;Title: The carboxyl-terminal half of type VII collagen,
A;Reference number: 148103; MUID:93271985; PMID:8499916
A;Accession: I84686
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A;Accession: I56328
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Toc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
JTitle: Dominant dystrophic epidermolysis bullosa: identification of a Gly Reference number: A55255; MUID:94224777; PMID:8170945
Contents: annotation
Comment: Prolines and lysines at the third position of the tripeptide reped and subsequently O-glycosylated.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231-131/Domain: Fibronectin type III repeat homology <FN1>
327-413/Domain: fibronectin type III repeat homology <FN2>
414-502/Domain: fibronectin type III repeat homology <FN3>
508-593/Domain: fibronectin type III repeat homology <FN4>
586-683/Domain: fibronectin type III repeat homology <FN6>
686-71/Domain: fibronectin type III repeat homology <FN6>
686-71/Domain: fibronectin type III repeat homology <FN6>
716-862/Domain: fibronectin type III repeat homology <FN7>
864-952/Domain: fibronectin type III repeat homology <FN8>
954-1045/Domain: fibronectin type III repeat homology <FN9:
1052-1219/Domain: von Willebrand factor type A repeat homol
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17-2944/Product: collagen alpha 1(VII) chain #status predicted <MAT>
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| Residues: A',1240-1246','G',1248-1250,'XE',1253-1255,'Q',1257,'E';2032,'C',2034-2041;
| Note: two reported peptides cannot be reliably located
| Greenspan, D.S.
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Dermatol. 99, 691-696,
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, 1992
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C;Comment: This protein is a sialoglycoprotein synthesized by alveolar ty pendent on the presence of calcium ions.
C;Superfamily: mannose-binding lectin; C-type lectin homology
C;Keywords: acetylated amino end; alveolar proteinosis; calcium; gaseous
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-247/Product: pulmonary surfactant protein A #status predicted <MAT>
F;27-99/Region: Collagen-like
                                                                                           F;126-245/Domain: C-type lectin homology <LCH> F;16/Modified site: acetylated amino end (Ser) (in
                                                                                                                                                                                                                                    A;Note: 12-Pro was also found
A;Note: two species of mRNA, which appear to be transcribed fr
A;Note: two species of mRNA, which appear to be transcribed fr
A;Note: the amino end of the mature protein is blocked
A;Note: the amino end of the mature protein is a complex of phospholipids
C;Comment: Tulmonary surfactant is a complex of phospholipids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:J03542; NID:9165705; PIDN:AAA31465.1; PID:9165706
A;Note: 12-Pro was also found
                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A; Accession: A29931
                                                                                                                                                                                                                                                                                                                                                                                                       R;Boggaram, V.; Qing, K.; Mendelson, C.R.
J. Biol. Chem. 263, 2939-2947, 1988
A;Title: The major apoprotein of rabbit pulmonary surfactant.
A;Reference number: A29931; MUID:88139348; PMID:2830270
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A; Residues: 1-210 <SHAPA
A; Cross - references: GB: 04671;
A; Cross - references: GB: 04671;
C; Superfamily: unassigned colla
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A;Accession: B44984
A;Status: preliminary
A;Molecula ****
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A; Residues: 1-247 <BOG>
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C;Date: 28-Apr-1993 #sequence_revision 28
C;Accession: B44944
R;Shamansky, L.M.; Pratt, D.; Boisvenue,
Mol. Biochem. Parasitol. 37, 73-86, 1989
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45 GLPGRDGRDG

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A;Gene: GDB:SFTPA1; SFTP1; SP-A; SP-A1
A;Cross references: GDB:119593; OMIM:1786
A;Map position: 10q22-10q23
C;Superfamily: mannor
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A:Note: part of the sequence was confirmed by protein sequencing
A:Note: the amino end of the mature protein, which was not identified,
A:Note: clones corresponding to two different proteins were sequenced.
C:Genetics:
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A;Title: Isolation and characterization of cDNA clones for the 35-kDa pulmonary surfacta A;Reference number: A25720; MUID:86250832; PMID:3755136
A;Accession: B25720
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A; Residues: 1-248 <FLO>
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N;Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associated
C:Species: Homo sapiens (man)
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A;Title: Isolation and characterization of cDNA clones for the 35-kDa pulmonary surfacts A;Reference number: A25720; MUID:86250832; PMID:3755136
A;Accession: A25720
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A;Cross-references: GDB:11
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                                                                                                                                                                                                                                                        superfamily: mannose-binding lectin; C-type lectin homology; Keywords: acetylated amino end; alveolar proteinosis; calcium; ga; 1-20/Domain: signal sequence #status predicted <SIG>
21-248/Product: pulmonary surfactant protein A #status predicted : 127-246/Domain: C-type lectin homology <LCH>
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N;Alternate names: pulmonary surfactant 32K apoprotein; pul
                                                                                                                                                          21/Modified site: acetylated amino end (Glu) (in mature form) #status predicted 30,33,36,42,54,57,63,76,79,82,91,97/Modified site: 4-hydroxyproline (Pro) #status
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Residues: 1-248 <FLO>
                                                                                                                                              /Binding site: carbohydrate
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                                Local Similarity
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                                                                                                                                                  pulmonary surfactant protein A precursor - rat
N;Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C;Accession: A29299; JS0034; S23183
R:Sano, K.; Fisher, J.; Mason, R.J.; Kuroki, Y.; Biochem. Biophys. Res. Commun. 144, 367-374, 1987 A;Title: Isolation and sequence of a cDMA clone f. A;Reference number: A29299; MUID:87213191; PMID:3
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Nature 325,
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C; Comment: Pulmonary surfactant is a complex of phospholipus C; Comment: This protein is a sialoglycoprotein synthesized by pendent on the presence of calcium ions.
C; Superfamily: mannose-binding lectin; C-type lectin homology C; Keywords: alveolar proteinosis; calcium; disulfide bond; ga: F; 1-17/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                            F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-248/Product: pulmonary surfactant protein A #status experimental <MPT>
F;28-102/Region: collagen-like
F;127-246/Domain: C-type lectin homology <LCH>
F;20,207/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;30/Modified site: 4-hydroxyproline (Pro) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Ross, G.F.; Meuth, J.; Ohning, B.; Kim, Y.; Whitsett, J.A. Biochim. Biophys. Acta 870, 267-278, 1986
A;Title: Purification of canine surfactant-associated glycoproteins A. Identification A;Reference number: A60142; MUID:86159848; PMID:3006781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: A93388; MUID:87115834; PMID:3808053
A;Contents: annotation; animal lectin domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 24-34; 95-101, 'x', 103-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Note: the authors translated the codon TTG for residue 60 as Pro A:Note: part of the sequence, including the amino end of the mature protein, was conf R:Liau, D.F.; Ryan, S.F.
Chem. Phys. Lipids 59, 29-38, 1991
A:Title: Purification of surfactant protein A from dog lung by reconstitution with su A:Reference number: A61227; MUID:92163993; PMID:1790579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Benson, B.; Hawgood, S.; Schilling, J.; Clements, J.; Damm, D.; Cordell, B.; White, Proc. Natl. Acad. Sci. U.S.A. 82, 6379-6383, 1985
A;Title: Structure of canine pulmonary surfactant apoprotein: cDNA and complete amino A;Reference number: A25296; MUID:86016705; PMID:3863100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Canis lupus familiaris (dog)
C; Date: 30-Sep-1987 *sequence_revision 30-Sep-1987
C; Accession: A25296; A61227; A60142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Pulmonary surfactant is a complex of phospholipids and proteins that lower This protein is a slaloglycoprotein synthesized by alveolar type II cells.
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49
                                                                                                                              100.0%;
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                                                                                                                                                       4.18;
                                                                                               Score 10; DB 1; Pred. No. 0.13; 0; Mismatches
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В.;

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A;Gene: GDB:SFTPA1; SFTP1; SP-A; SP-A1
A;Cross-references: GDB:119593; OMIM:178630
A;Map position: 10922-10923
A;Introns: 58/1; 98/1; 124/1
C;Superfamily: mannose-binding lectin; C-type lectin homology
F;127-246/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pendent on the presence of calcium ions.

C:Comment: Two species of mRNA, which probably are transcribed from a single gene, have C:Comment: Size heterogeneity of these proteins arises from posttranslational modificati C:Keywords: alveolar proteinosis; calcium; gaseous exchange; glycoprotein; hydroxyproling; 1-20/Openain: signal sequence #status predicted <SIG>F:21-248/product: pulmonary surfactant protein A #status experimental <MAT>F:37-109/Region: collagen-like
F:127-246/Domain: C-type lectin homology <LCH>F:21/Binding site: carbohydrate (Asn) (covalent) #status absent
F:30,33,36,43,54,57,63,67,70,76/Modified site: 4-hydroxyproline (Pro) #status experiment
                                                                                                                                                                                                                                                                                                                      A;Reference number: I51921; MUID:92198680; PMID:1372511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Contents: 0.9 kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
                                                                                                                                                                                                                         Genetics:
                                                                                                                                                                                                                                      Cross-references:
               Matches
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Reference number: S23183; MUID:92298987; PMID:1606951
Accession: S23183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Comment: Pulmonary surfactant is a complex of phospholipids and proteins that lowers to Comment: This protein is a sialoglycoprotein synthesized by alveolar type II cells. It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: DNA
Residues: 1-32 <LAC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: mRNA
Residues: 1-248 <FI
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                                                                                                                                                                                                                                                                                                                                                                        Respir. Cell Mol. Biol. 6,
                                  Боса I
                                                                                                                                                                                                                                                                                                                                                     Characterization of a second human pull
                                                                                                                                                                                                                                                                                          preliminary; translated from GB/EMBL/DDBJ
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             10;
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MUID:89000785; PMID:2901856
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                          Score 10;
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2003, 15:06:31

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A;Title: Murine pulmonary surfactant SP-A gene: cloning, sequence, and transcriptiona A;Reference number: A48853; MUID:93072386; PMID:1443158
A;Contents: DBA/2J
A;Accession: A48853
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A; Residues: 1-248 < KOR>
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A48853
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                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Mus muscu
C; Date: 19-Dec-1993
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                                                                           Conservative
                                                                                                                                                               GB:S48768; NID:g260452; PIDN:AAB24274.1; PID:g260453 tracted from NCBI backbone (NCBIN:118740, NCBIP:118741) ose-binding lectin; C-type lectin homology
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                                                                     4.1%; Score 10; DB 100.0%; Pred. No. 0. ative 0; Mismatches
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0.13;
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618.141 Million cell updates/sec
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sp_phage:*
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sp_fungi:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
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sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_mnc:*
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             289
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Q9N1X4
002842
057451
Q919Q7
Q9TT06
Q9N0G1
Q9SQ11
Q9SQ11
Q9SQ11
Q9SQ11
Q9SQ19
Q919Q9
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Q9UCJ3
Q19813
Q9ACN2
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OBtcdB homo sapien
Ognix4 sus scrofa
O22842 papio cynoc
O57451 gallus gall
O91997 carassius a
O9tt06 ovis aries
O9n091 equus cabal
O95188 equus cabal
O95188 equus cabal
O95181 mus musculu
O98ta4 gallus gall
O9199 cyprinus ca
O8wp36 suberites d
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Q9ucj3 homo sapien
Q19813 caenorhabdi
Q9acn2 streptococc
Q8tcd8 homo sapien
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Best Local S
Matches 62
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ database;
EMBL; BC023068; AAH23068.1; -.
EMBL; BC025174; AAH25174.1; -.
Hypothetical protein,
Hypothetical protein,
SEQUENCE 243 AA; 25420 MW; 498129CD051DB97B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to DKFZP586B0621 protein (Hypothetical 25.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8R002;
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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62; Conserv
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                                                                     243
                                                                                                                                                             Conservative
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100.0%;
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1 Q63074
6 Q9HZ09
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745313
Q9BQY7
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6 Q9RD9
6 P74713
Q9GLV5
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                                                                                                                                                        Score 62; DB 11;
Pred. No. 4.8e-52;
0; Mismatches 0;
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O9dyng rattus norv
O9dyng brachydanio
O9swq3 artemisla a
O9ak64 streptomyce
P90679 arenicola m
O60438 mus musculu
O60709 mus musculu
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O60708 mus musculu
O60708 rattus norv
O903081 caenorhabdi
O903081 caenorhabdi
O903087 rattus norv
O903074 rattus norv
O903074 rattus norv
O903074 pseudomonas
O90477 homo sapien
O9cvj2 mus musculu
O9cvj2 mus musculu
O9rd99 streptomyce
O9jxb1 neisseria m
O9wv2 neisseria m
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O9wv2 neisseria m
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Best Local :
                                                                                               Waterston R.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; U55373; AAC25888.1; -
InterPro; IPR000087; Collagen.
InterPro; IPR002486; Col_outicle_N.
Pfam; PF01391; Collagen; 3.
Pfam; PF01484; Col_cuticle_N; 1.
SEQUENCE 289 AA; 28740 MW; DFFB78B2B34B29DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson R., Bentley D., Gattung S.;
"The sequence of C. elegans cosmid F26F12.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE-99069613; PubMed-9851916;
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Q19813;
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Science 282:2012-2018(1998).
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01-NOV-1996 (TrEMBLrel
01-JUN-2002 (TrEMBLrel
F26F12.1 protein.
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
MCBI_TaxID=6239;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome sequence of the nematode C. elegans: a platform for nvestigating biology. The C. elegans Sequencing Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93142849; PubMed=8424457; Crouch E., Persson A., Chang D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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Am. J. Pathol. 142:241-248(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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27 AA; 2696 MW;
                Conservative
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Catarrhini;
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DB 5; Lc.
3. 0.026;
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o. 0.0028;
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i; Hominidae; Homo.
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         Indels
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Gaps
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Best Local
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                                                                                                             Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases EMBL; BC022318; AAH22318.1; -
Hypothetical protein.
SEQUENCE 375 AA; 37655 MW; CCB7375D3C86421A CRC64;
                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 37,7 kDa protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          TISSUE-LUNG
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8TCD8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8TCD8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01391; Collagen; 1.

Pfam; PF00746; Gram_pos_anchor; 1.

PRINTS; PR00015; GPOSANCHOR.

TIGRERAMS; TIGR01167; LPXTG_anchor; 1.

PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9ACN2;
01-JUN-2001
01-JUN-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Streptococcaceae; Streptococcus.
NCBI_TaxID-1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fransmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21097281;    PubMed=11158359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SclB protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9ACN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Natmore A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 GPRGEAGPAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222
                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
GLPGRDGRDGR 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPRGEAGPAGP 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGPRGEAGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGPRGEAGPAG
                                                            4.5%;
ilarity 100.0%;
Conservative
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l (TrEMBLrel. 17,
2 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31833 MW;
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100.0%; Pred. No.
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                                                                         Score 11; pred. No.
                                                            0;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Patarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57EBDC244DF17600 CRC64;
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                                                          Mismatches
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                                                                            DB 4;
. 0.033;
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                                                                                                                                                                                                                                                                                                                                                  Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 306;
0.027;
hes 0; Indels
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Best Local Similarity 100
Matches 11; Conservative
               SEQUENCE FROM N.A. TISSUE-KIDNEY; Gao E., Wang Y., Mc Submitted (MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                     002842;
01-JUL-1997
01-JUL-1997
01-JUN-2002
                                                                                                             MEDLINE-97053398; PubMed-8897910;
Gao E., Wang Y., McCormick S.M., Li J., Seidner S.R.,
"Characterization of two baboon surfactant protein A can, J. Physiol. 271:L617-L630(1996).
                                                                                                                                                                                                                                                                   01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Surfactant protein A2 (Fragment).
Papio cynocephalus (Yellow baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.

MCBI_TaxID-9556;
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                               TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                002842
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Pfam; PF00059; lectin_c; 1.
ProDom; PD000007; Collagen; 2.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           localisation and tissue distribution.",
Immunol. 164:1442-1450(2000).
EMBL; AF132496; AAF22145.2;
HSSP; P35247; 1808.
InterPro; IPR000087; Collagen.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20109098; PubMed-10640760;
MEDLINE-20109098; PubMed-10640760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porcine Lung Surfactant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      van Eijk M., Haagsman
Lawson P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9N1X4;
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CT-2000 (TIEMBLrel. 15, Last sequence update)
UN-2002 (TIEMBLrel. 21, Last annotation update)
Burfactant protein D precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46
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Wang Y., McCormick S.M., Li J., Seidner S.R., Mendelson
ed (MAY-1997) to the EMBL/GenBank/DDBJ databases.
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21
378
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378 L
; 37986 MW;
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Cetartiodactyla; Suina; Suidae;
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Pred. No.
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LUNG SURFACTANT PROTEIN D.
3504E8C1E56C341D CRC64;
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0.033;
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                                                                                                                                    genes
                                                                                                                                                    Mendelson
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Sus.
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RESULT 9
Q9197
ID Q919
AC Q919
DT 01-0
DT 01-0
DT 01-0
CT MANN
GN MBL.
OS Cara
OC Euka
OC Euka
OC Cypr
OX NCB1
RN (1)
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057451
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                                                        Q919Q7 PRELIMINARY;
Q919Q7;
Q919Q7;
01-OCT-2000 (TrEMBLrel. 15, C
01-OCT-2000 (TrEMBLrel. 15, L
01-JUN-2002 (TrEMBLrel. 21, L
Mannose binding-like lectin p
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Best Local s
Matches 10
InterPro; IPR000087; Collagen.
InterPro; IPR001304; Lectin_C.
Pfam; PF001391; Collagen; 1.
Pfam; PF00059; lectin_C; 1.
ProDom; PD000007; Collagen; 1.
SMART; SM00034; CLECT; 1.
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EMBL; AF003896; AAB61294.1; -.
ThterPro; IPR000087; Collagen.
                                                                                                                                                                                                                      Lectin.
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                PROSITE;
PROSITE;
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01-JUN-1998
01-JUN-2002
                                                                                                                                                                                                                                                                                                                     Laursen S.B.;
Submitted (AUG-1997) to the
EMBL; AF022226; AAB94071.1;
HSSP; P19999; 1YTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       057451;
                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                      STRAIN-WHITE LEGHORN;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mannan-binding
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
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ProDom; PD000007; Collagen;
NON_TER 57 57
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                                                                                                                                                           45 GLPGRDGRDG
                                                                                                                                                                                    10;
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10; Conserv
                                                                                                                                                  GLPGRDGRDG
                                                                                                                                                                                                                                             PS00615; C_TYPE_LECTIN_1; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLPGRDGRDG
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238 p
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                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 lectin (Fragment).
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25645 MW;
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                                                                                                                                                                                                     4.18;
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                                                                                                                                                                                                                                                                                                                                                    TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                           21,
21,
                                                      Last sequence update)
Last annotation update)
precursor (Fragment).
                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ databases
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Last sequence update)
Last annotation update)
                                                                                                                                                                                          Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 10;
Pred. No.
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                                                                                                                                                                                 Mismatches
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                                                                                                    246
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                   Vertebrata; Euteleostomi;
Ostariophysi; Cypriniform
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if sepressed at high level in spleen, and the deduced primary

I servicture predicts affinity for galactose.";

I Immunogenetics 51:955-944(2000).

REMBL, AF227739; AAF63470.1; -.

PREMBL, AF227739; AAF63470.1; -.

RISSP: P35247; 1808.

RICTETFO; IPRO01304; Lectin_C.

PREMB, PF001391; Collagen.

PREMB, PF001391; Collagen; 2.

DR Pfam; PF001391; Collagen; 2.

DR Pfam; PF001394; Clectin_C; 1.

DR SMART; SM00034; CLECT; 1.
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Pietschmann S.M., Pison U.;
"CDNA cloning of ovine pulmonary Sp-A, St
two different sequences for Sp-B.";
Am. J. Physiol. 278:L/65-L/78(2000).
EMBL; AF211856; AAF118995.1;
EMBL; AF076633; AAF31148.1;
HSSP; P22897; LEGG.
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O1-MAY-2000 (TrEMBLrel. 13, L
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MEDLINE-20215262; PubMed-10749753;

Braems G.A., Yao L.-J., Inchley K., Brickenden A

Grolla A., Challis J.R.G., Possmayer F.;

Grolla A., Challis J.R.G., Possmayer F.;

O'Ine surfactant protein cDNAs: use in studies

and maturation after prolonged hypoxemia.";

Am. J. Physiol. 278:L754-L764(2000).
                                                                                                                                                                                                                                               InterPro;
InterPro;
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Ovis aries (Sheep).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovoidae; Caprinae; Ovis.
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pulmonary surfactant protein A (Pulmonary surfactant-associated
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PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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TISSUE-LIVER;
                                                                                                    erPro; IPRO00087; Collagen.
ErPro; IPRO01087; Collagen.
Collagen; 2.
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C_TYPE_LECTIN_1; 1.
C_TYPE_LECTIN_2; 1.
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DR Inter
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weber B.I.L. Hospes R., Gortner L.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; AF400580; AAL077690.1; -.
R Interpro; IPR000087; Collagen.
R Interpro; IPR001304; Lectin_C.
R Pfam; PF01391; Collagen; 2.
R Pfam; PF01391; Collagen; 2.
R Pfam; PF00059; lectin_C; 1.
R PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
R PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
SEQUENCE 248 AA; 25047 MW; B71133E005C9A5C1 CRC64;
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Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS000615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 248 AA; 26000 MW; BBE12EFBI
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01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                         Pulmonary surfactant associated profile A. Equus caballus (Horse).
Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Q9NOG1;
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Mammalia; Eutheria;
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Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lobo S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 100
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLPGRDGRDG 54
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10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata;
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100.08; Pr/
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                   Gortner L.;
:he EMBL/GenBank/DDBJ databases
.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     juine pulmonary surfactant proteins.";
the EMBL/GenBank/DDBJ databases.
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Last sequence update)
Last annotation update)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BBE12EFB05C2B8D1 CRC64;
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0.21;
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0.21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                         Euteleostomi;
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Q98TA4
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                                RESULT 14
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furino M., Aono H., Baldarelli R., Barsh G.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furino M., Aono H., Baldarelli R., Barsh G.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashizaki Y.:
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Q9CQI1
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                                                                                                                                                Query Match
Best Local :
                                                                                                                                    Matches
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Best Local S
Matches 10
    Q98TA4
                                                                                                                                                                               Pfam; PF01391; Collagen; 2.

Pfam; PF00059; lectin_c; 1.

SMART; SM00034; CLECT; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a fu

Mature 409:685-690(2001).

EMBL; AK011333; BAB27551.1; -

EMBL; AK004620; BAB23416.1; -

EMBL; AK004788; BAB23565.1; -
                                                                                                                                                                                                                                                                         InterPro; IPR000087; Collagen.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                      MGD; MGI:109518; Sftpa.
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01-JUN-2001
01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE-EMBRYO, AND LUNG;
MEDLINE-2108566; PubMed-11217851;

MEDLINE-2108566; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Surfactant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
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                                                                                                    45
                                                                                                                                 . Similarity
10; Conserv
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                                                                                      GLPGRDGRDG
                                                                        GLPGRDGRDG
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2 (TrEMBLrel. 21, La
associated protein
 PRELIMINARY;
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                        49
                                                                                                    54
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Rodentia;
                                                                                                                                             100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 17, Created)
. 17, Last sequ
. 21, Last anno
                                                                                                                                             .08;
                                                                                                                           Score 10; DB; Pred. No. 0.2
                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                      full-length mouse cDNA collection.";
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleóstomi;
Sciurognathi; Muridae; Murinae; Mus
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254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248
                                                                                                                                                     DB 11; Length 248;
                                                                                                                                         0.21;
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0.21;
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RESULT
Q919Q9
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Best Local
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                                  MEDLINE-20456722; PubMed-11003389; Vitved L., Holmskov U., Koch C., Teisner B., H "The homologue of mannose-binding lectin in the is expressed at high level in spleen, and the structure predicts affinity for galactose."; Immunogenetics 51:955-964(2000).

EMBL; AF227737; AAF63468.1; -.
HSSP, P35247; 1808.
                                                                                                                                                                                                                                             Q919Q9;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2002 (TrEMBLrel. 21,
ASSP; P35247; IDVU.
InterPro; IPR000087; Collagen.
InterPro; IPR001304; Lectin_C.
PR01391; Collagen; 2.
                                                                                                                                                                  Cyprinus carpio (Common carp).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform
Cyprinidae; Cyprinus.
NCBI_TaxID-7962;
                                                                                                                                                                                                                                     Mannose binding-like lectin
                                                                                                                                                                                                                                                                                                091909
                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
SEQUENCE
                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000007; Coll;
SMART; SM00034; CLECT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q98TA4;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lectin; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01391; Collagen; Pfam; PF00059; lectin_c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is expressed at high level in spleen, and the structure predicts affinity for galactose."; Immunogenetics 51:955-964(2000). EMBL; AF231714; AAK30298.1; -... EMBL; P19999; IYTT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000087;
InterPro; IPR000005;
InterPro; IPR001304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=20456722; PubMed=11003389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mannose-binding lectin protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hitved L., Holmskov U., Koch C., Telsner The homologue of mannose-binding lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vitved
                                                                                                                                                                                                                                                                                                                       15
                                                                                                                                                                                                                                                                                                                                                        47 GLPGRDGRDG
                                                                                                                                                                                                                                                                                                                                                                                45
                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                     GLPGRDGRDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                22
234
254 AA;
                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                21 P
254 M
234 D
27376 MW;
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HTHAraC.
                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lectin_C
                                                                                                                                                                                                                                                                                                                                                                                                                           4.18;
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Last annotation update)
                                                                                                                                                                                                                                     precursor.
                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                               Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MANNOSE-BINDING LECTIN PROTEIN D -> V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence up
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DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Lectin; Signal 1 23 POTENTIAL.
ET SIGNAL 1 24 256 MANNOSE BINDING-LIKE LECTIN.
ET CHAIN 235 235 S > T.
SQ SEQUENCE 256 AA; 26934 MW; D019291D1167730D CRC64;
Query Match
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps
Oy 45 GLPGRDGRDG 54
Db 45 GLPGRDGRDG 54
CSearch completed: June 18; 2003, 15:05:52
Job time: 91 secs
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-09-336-536-13
US-09-336-536-13
US-09-336-536-13
US-09-336-536-13
US-09-336-536-13
US-09-336-536-13
US-09-318-20-4
US-09-318-20-4
US-09-500-811-12
US-09-500-811-12
US-09-500-811-12
US-09-511-942-15
US-09-211-942-15
US-09-530-423-2
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10, Appl

6, Appl

13, Appl

13, Appl

5, Appl

190, App

4, Appl

21, Appl
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US-09-336-536-3
; Sequence 3, Application US/09336536
; Patent No. 6406884
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## ALIGNMENTS

RESULT 1 US-09-140-804-2

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GENERAL INFORMATION:

APPLICANT: Sheppard, Paul O.

APPLICANT: Humes, Jacquelline M.

TITLE OF INVENTION. ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS

FILE REFERENCE: 97-49

CURRENT APPLICATION NUMBER: US/09/140,804

CURRENT FILLING DATE: 1998-08-26

EARLIER APPLICATION NUMBER: 60/056,983

EARLIER APPLICATION NUMBER: 05/056,983

NUMBER OF SEQ ID NOS: 47

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 243
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; ORGANISM: Homo
US-09-140-804-2
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Best Local Similarity
Matches 243; Conserv
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| VFA 243
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100.0%; F
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Pred. No. 1.6e-218;
); Mismatches 0;
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GENERAL INFORMATION:

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CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 228
TYPE: PRT
ORGANISM: Homo sapiens
US-09-336-536-4
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APPLICANT: MCKBY, C.
APPLICANT: MCKBY, C.
APPLICANT: BOSSONG, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THE
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATENTIN Ver. 2.0
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Matches 228
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Patent NO. 6406884
GEMERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES
FILE REFERENCE: 7853-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-336-536-3
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241 VFA 243
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11arity 100.0%; Pred. No. 1.4e-204;
Conservative 0; Mismatches 0;
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CURRENT INVENTALIANN.

APPLICANT: Watson, James D.

APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Orrust, Rene
APPLICANT: Orrust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: And Methods For Their Use
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT APPLIANG DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FASTED for Windows Version 3.0
LENGTH: 243
TYPE: PRT
CORANISM: Rat
US-09-188-930-295
Query Match
Best Local Similarity
Thes 70; Conserve
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APPLICANT: Leaby, K.

APPLICANT: MCRAY, C.

APPLICANT: MCRAY, C.

TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

FILE REFERENCE: 7853-144

CURRENT APPLICATION NUMBER: US/09/336,536

CURRENT APPLICATION NUMBER: US/09/336,536

CURRENT FILING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 75

SEQ ID NO 7

FENORUM: 100
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-336-536-7
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US-09-336-536-7
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NO. 6406884
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                           28.8%;
100.0%;
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100.0%; Pred. No. 9.7e-112;
tive 0; Mismatches . 0;
        Score 70; DB 4; 1: Pred. No. 1.6e-57 0; Mismatches 0
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                                     Length 243;
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APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
SOUNBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 243
TYPE: PRT
ORGANISM: Mus musculus
US-09-336-536-10
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APPLICANT: MCKBY, C.
APPLICANT: BOSSONE, S.
APPLICANT: BOSSONE, S.
FILE REFERENCE: 7853-144
CURRENT APPLICATION UNMEER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATENTIN Ver. 2.0
LENGTH: 228
TYPE: PRT
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                                                                                                           Query Match
Best Local
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US-09-336-536-11
                                                                                                Matches
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US-09-336-536-11
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                                                                                                                                                                                                                                                                                                                              sequence 10, Application US/09336536
Patent No. 6406884
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Best Local Similarity
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                                                                                              Local Similarity
nes 62; Conserv
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                                                                                     25.5%; Score 62; DB 4;
ilarity 100.0%; Pred. No. 4.5e-:
Conservative 0; Mismatches
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ilarity 100.0%;
Conservative (
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; Pred. No. 4.2e-50;
rematches 0; Indels
                                                                                     4.5e-50;
hes 0;
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US-09-336-536-13
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Best Local
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US-09-336-536-6
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Sequence 13, Application US/09336536

Patent No. 6406884

GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF FILE REFERENCE: 7853-144
CCURRENT APPLICATION NUMBER: US/09/336,536
CURRENT APPLICATION NUMBER: US/09/336,536
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Leiby, K.
APPLICANT: Heaby, C.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 60
TYPE: PRT
ORGANISM: Homo sapiens
US-09-336-536-6
                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Mus musculus US-09-336-536-14
                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 14
LENGTH: 128
TYPE: PRT
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Conserv
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APPLICANT: MCKBY, C.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
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Patent No. 6406884
                                                                                                                                                                                                                                                    INFORMATION:
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100.0%; Pred. No. 4.4e-40;
^^ Mismatches 0;
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100.0%; Pred. No.
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o. 9.6e-49;
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-09-336-536-5

Matches

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; ORGANISM: Homo sapiens
US-09-336-536-5
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: ORGANISM: Mus musculus
US-09-336-536-13
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CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 5
                                                                                                                                                                                                                                                                                                                                                     Sequence 190, Application US/09227357
Patent No. 6342581
                                                                                                                                                                                                                                                                                  ENERAL INFORMATION:
APPLICANT: Fischer et al.
FITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: PZ010p1
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Patent No. 6406884
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Best Local Similarity
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ARLIER APPLICATION NUMBER: PCT/US98/13684
ARLIER FILING DATE: 1998-07-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
                                                                                                                                                                                                                                                                        RRENT APPLICATION NUMBER: US/09/227,357
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hes 15; Conserv
                 R APPLICATION NUMBER: 60/052,803
R FILING DATE: 1997-07-08
R PAPPLICATION NUMBER: 60/052,732
R FILING DATE: 1997-07-08
R APPLICATION NUMBER: 60/051,931
R FILING DATE: 1997-07-08
                                                                                                             APPLICATION NUMBER: 60/051,929 FILING DATE: 1997-07-08
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                                                                                                                                                                                                  APPLICATION NUMBER: 60/051,926 FILING DATE: 1997-07-08
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1 MRPLLVLLLGLAAG 15
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100.0%; Pred. No. 6.3e-33;
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COTHER INFORMATION:
US-09-227-357-190
                                                                            Query Match
Best Local :
                                                                Matches
                                                                                                                                                                                                                                                                                                       SEQ ID NO 190
                                                                                                                                                                                                                                                LENGTH: 128
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
                                                                                                                                                                 NAME/KEY: SITE
                                                                                                                                                                                                              NAME/KEY: SITE LOCATION: (127)
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                                                                                                                                                                                                                                                                                                                                          PARLIER APPLICATION NUMBER: 60/
PARLIER FILING DATE: 1997-09-12
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59 GLPGRDGRDGR 69
                           45 GLPGRDGRDGR 55
                                                              l Similarity
11; Conser
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FILING DATE: 1997-08-18
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100.0%; Pr
1.72 0;
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1997-08-18
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                                                                      Score 11;
Pred. No.
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                                                        Mismatches
                                                                    DB 4;
. 0.0074;
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RESULT 12 JS-09-227-357-190

EARLIER EARLIER

Length 128; Indels

0, Gaps

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Query Match Best Local

LENGTH: 15 TYPE: PRT

Matches

US-08-931-820-4

cent No.

INFORMATION:

4, Application US/08931820 5. 6010863

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                                                                                                                                                                                            APPLICANT: QVIST, Per APPLICANT: Bonde, Martin TITLE OF INVENTION: A Method for TITLE OF INVENTION: Method and (TITLE OF INVENTION: Disorders A: NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
ADDRESSE: Darby 6 Darby PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           quence 21, Applitent No. 6110689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acids
                                                                                                                                                          STREET: 805 Th
CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA;
                                                                                                                          ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1055
OTHER INFORMATION: /label= modified
OTHER INFORMATION: /note= "Ala may be Pro"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      680 GAPGEKGEGG 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 GAPGEKGEGG 69
                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                  Application US/08963825
                                                                                                                                                                                 805 Third Avenue
                                                                                                                                        USA
                         PatentIn Release #1.0, Version #1.25
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in Body Fluids, A Test Kit and Means for
US/08/963,825
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to Diagnose the Presence of
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US-09-500-811-21
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Patent No. 632331
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                         NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
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ORIGINAL SOURCE:
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LENGTH: 1078 amino acids
TYPE: amino acid
TOPOLOGY: linear
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
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FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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Local Similarity 100.0%;
es 10; Conservation
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REGISTRATION NUMBER:
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Pred. No.
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Page 6

INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
ONLECULE TYPE: protein
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
US-09-500-811-21 Search completed: June 18, 2003, 15:07:04 Job time : 27 secs В Query Match
4.1%; Score 10; DB 4; Length 1078;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 60 GAPGEKGEGG 69 ||||||||| 681 GAPGEKGEGG 690 0; Indels 0; Gaps 0;

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd
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          APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Andrey
APPLICANT: Hillan, Kenneth
APPLICANT: Hillan, Kenneth
APPLICANT: Hopler, Mary
APPLICANT: Mapler, Mary
APPLICANT: Mapler, Mary
APPLICANT: Mood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
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FILING DATE:
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US-10-140-921-362
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Minimum DB

Word size Searched:

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000

Post-processing: Listing first 45 summaries

Published\_Applications\_AA:\*

Title: Perfect score: Sequence:

US-09-943-851A-42

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protein -

protein search, using sw model

9

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

417779 seqs, 108206813 residues

Result

Score

Query Match

Length

DB

SUMMARIES

10: 11: 12: 13:

100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0

US-09-944-413-42
US-09-944-805-42
US-09-944-907-42
US-09-944-907-42
US-09-944-292-42
US-09-944-629-42
US-09-944-629-42
US-10-121-049-362
US-10-123-904-362
US-10-176-918-362
US-10-140-474-362
US-10-140-474-362
US-10-140-474-362
US-10-140-1002-362

Section Section Section 1

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PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR APPLICATION NUMBER: 60/06935
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
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US-09-944-403-42
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PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/944,403
CURRENT FILING DATE: 2001-09-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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APPLICANT: Botst
APPLICANT: Eaton
                           APPLICATION NUMBER: 60/070,440
                                                                                APPLICATION NUMBER: 60/069,873 FILING DATE: December 17, 1997
FILING DATE: January 5, 199
APPLICATION NUMBER: 60/074
                                               APPLICATION NUMBER: 60/068, FILING DATE: December 18, 1
                                                                                                              APPLICATION NUMBER: 60/069,870
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US20020165143A1
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Wood, William
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; TYPE: PRT ; ORGANISM: Homo Sapien US-09-944-413-42

SEQ ID NO 42

LENGTH: 243

PRIOR APPLICATION NUMBER: PCT/US01/06520 PRIOR FILING DATE: February 28, 2001

February 28, OS: 120

DATE: December DATE: July 28,

APPLICATION NUMBER: PCT/US00/08439
FILING DATE: March 30, 2000
APPLICATION NUMBER: PCT/US00/14042
FILING DATE: May 22, 2000

FILING DATE: March 2,

APPLICATION NUMBER:

PCT/US00/05841

2000

2000

APPLICATION NUMBER: PCT/US00/04414

APPLICATION NUMBER: PCT/US00/03565 FILING DATE: February 11, 2000

APPLICATION NUMBER: PCT/US99/30095 FILING DATE: December 16, 1999

FILING DATE: December1,

APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020156004A1ember 30,
APPLICATION NUMBER: PCT/US99/28301

1999 1999

FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020156004Alember 30,

APPLICATION NUMBER: PCT/US99/12252 FILING DATE: June 22, 1999 APPLICATION NUMBER: PCT/US99/21090

FILING DATE: December 16, 1998
APPLICATION NUMBER: 09/218,517
FILING DATE: December 22, 1998
APPLICATION NUMBER: 09/254,311
FILING DATE: March 3, 199
APPLICATION NUMBER: PCT/US99/12252

FILING DATE: December 1, 19 APPLICATION NUMBER: 09/216, APPLICATION NUMBER: PCT/US98, FILING DATE: December 1, 1991

1998

/25108

FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/146,222
FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
FILING DATE: September 16,000

APPLICATION NUMBER: 60/112,850

December February

APPLICATION NUMBER: 60/

/113,296 22, 1998

FILING DATE:

APPLICATION NUMBER: 60/074,086

January

APPLICATION NUMBER: 60/070,440

FILING DATE: December APPLICATION NUMBER: 60/068,

APPLICATION NUMBER:

December

60/069,702 er 16, 1997 60/069

PLICATION NUMBER: 60,

/690

FILING DATE:

APPLICATION NUMBER: 6

/074, /075,

APPLICATION NUMBER: 6

ILING DATE: LING DATE:

APPLICATION NUMBER:

PCT/US00/20710 PCT/US00/32678

APPLICATION NUMBER:

Query Match

Matches

Local Similarity les 243; Conserv

100.0%; ilarity 100.0%; Conservative 0;

Score 243; DB 9; Pred. No. 7.9e-202; ; Mismatches 0;

Length 243; Indels

0;

1 MRPLLYLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG

PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: June 2

APPLICATION NUMBER: 09
FILING DATE: March 3,

PRIOR FILING DATE: December 16

APPLICATION NUMBER: 09/216,021 FILING DATE: December 1,

FILING DATE: September 16, 1998 APPLICATION NUMBER: PCT/US98/25108

NUMBER: PCT/US98/19330 September 16, 1998

APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: July 28

July 28,

60/146,222

APPLICATION NUMBER:

December

60/112,850 113,296

NUMBER: 60/074,092

LING DATE: December PLICATION NUMBER: 60/

APPLICATION NUMBER: 0: FILING DATE: December

09/218,517 per 22, 1998 09/254,311

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181 FFGGWPKPASLSGGANVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP 240
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US-09-944-896-42
; Sequence 42, Ap
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PRIOR APPLICATION NUMBER: 60/074,
PRIOR FILING DATE: February 9, 19
PRIOR APPLICATION NUMBER: 60/074,
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PRIOR APPLICATION NUMBER: 60/069,
PRIOR FILING DATE: December 17, 1
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PRIOR FILING DATE: December
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PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/06935
PRIOR APPLICATION NUMBER: 60/06935
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CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1
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                                                                             JR APPLICATION NUMBER: 725, 1998
JR APPLICATION NUMBER: 60/112,850
DR FILING DATE: December 16, 1998
OR APPLICATION NUMBER: 60/113,296
OR APPLICATION NUMBER: 60/113,296
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                           APPLICATION NUMBER: FILING DATE: Septem
                                                  APPLICATION NUMBER: 6 FILING DATE: July 28,
 FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/069,694 FILING DATE: December 16, 1997
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US20020168715A1
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Roy, Margaret
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Hillan, Kenneth
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121 121 ; TYPE: PRT ; ORGANISM: Homo Sapien US-09-944-403-42

LENGTH:

243

ID NO 42

PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR TILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEO ID NOS: 120

APPLICATION NUMBER: PCT/US00/20710 FILING DATE: July 28. 2000

FILING DATE: February 22, 2000
APPLICATION NUMBER: PCT/US00/05841
FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/US00/08439
FILING DATE: March 30, 2000
APPLICATION NUMBER: PCT/US00/14042

APPLICATION NUMBER: PCT/US00/04414

February December 16, December1,

PLICATION NUMBER: PCT/US00/03565

DATE:

APPLICATION NUMBER: PCT/US99/30095

FILING DATE: No. US20020165143A1ember APPLICATION NUMBER: PCT/US99/28301

APPLICATION NUMBER: PCT/US99/

/28313

30,

APPLICATION NUMBER: PCT/US99/28409
FILING DATE: NO. US20020165143Alember 30, 1999

FILING DATE: September

APPLICATION NUMBER:

PLICATION NUMBER: 22, 1999
POLICATION NUMBER: PCT/US99/21090
POLICATION NUMBER: PCT/US99/21090

Query Match Best Local Matches

Local Similarity les 243; Conserv

100.0%; Score 243; DB 9; 11arity 100.0%; Pred. No. 7.9e-202; Conservative 0; Mismatches 0;

Length 243; Indels

0;

Gaps

Mismatches

1 MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGRDGAPG

MRPLLVLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGRDGAPG

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US-09-944-944-42
                             Sequence 42, Application US/09944944
Patent No. US20020173463A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-896-42
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PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR APPLICATION NUMBER: PCT/US00/06439
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: MAY 22, 2000
PRIOR FILING DATE: MAY 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: FEBTUARY 28, 2001
PRIOR FILING DATE: FEBTUARY 28, 2001
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PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: NO. US20020168715A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: NO. US20020168715A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
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ENGTH: 243
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PRIOR FILING DATE: March 3,
PRIOR APPLICATION NUMBER: PC
PRIOR FILING DATE: June 22,
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                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: December 16, 1999
APPLICATION NUMBER: PCT/US00/03565
FILING DATE: February 11, 2000
APPLICATION NUMBER: PCT/US00/04414
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FILING DATE: December 16, 1998
APPLICATION NUMBER: 09/218,517
FILING DATE: December 22, 1998
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PRIOR FILING LANGE PRIOR FILING LANGE PRIOR APPLICATION NUMBER: U. 1998 PRIOR APPLICATION UMBER: 09/218,517 PRIOR FILING DATE: December 22, 1998 PRIOR PILING DATE: December 22, 1998 PRIOR FILING DATE: March 3, 1999 PRIOR FILING DATE: March 3, 1999 PRIOR APPLICATION NUMBER: PCT/US99/12252 PRIOR APPLICATION NUMBER: PCT/US99/12252 PRIOR FILING DATE: June 22, 1999 PRIOR FILING DATE: June 22, 1999 PRIOR FILING DATE: MUMBER: PCT/US99/12090 PRIOR FILING PRIOR F
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PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/060,017
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: TANNER: 150/070,440
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PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
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PRIOR FILING DATE: December 11, 1997
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PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
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PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,08
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PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069, 696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 694
PRIOR FILING DATE: December 16, 1997
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,944
CURRENT FILING DATE: 2001-09-26
CURRENT FILING DATE: 2001-09-26
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APPLICATION NUMBER: PCT/US98/19330

FILING DATE: September 16, 1998

APPLICATION NUMBER: PCT/US98/25108

FILING DATE: December 1, 1998

APPLICATION NUMBER: 09/216,021

FILING DATE: December 1, 1998

APPLICATION NUMBER: 09/216,021
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APPLICATION NUMBER: 60/112,850
FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
FILING DATE: December 22, 1998
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FILING DATE: December 22, 1998
FILING DATE: July 28, 1000
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Napier, Mary
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Tumas, Daniel
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Grimaldi, Christopher
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APPLICANT: Wood,William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,907
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 09/866,028
INUMBER OF SEQ ID NOS: 120
SEQ ID NO 42
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-907-42
PRIOR APPLICATION UNMBER: 2001-08-31
PRIOR FILING DATE: 2001-08-09-866,028
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 42
LENGTH: 243
TYPE: The second of the seco
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US-09-944-929-42
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APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,929
CURRENT FILING DATE: 2001-08-31
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243; Conserv
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Gurney, Austin
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Goddard, Audrey
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Napier, Mary
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100.0%; Pred. No. 7.9e-202;
tive 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Baker, Ke
APPLICANT: Botstein
APPLICANT: Eaton,Da
APPLICANT: Feirara,
APPLICANT: Filvarof,
APPLICANT: Gerritse

APPLICANT: APPLICANT:

Godowski, Paul Grimaldi, Christopher

Gerritsen, Mary Goddard, Audrey Filvaroff, Ellen

Gurney, Austin Hillan, Kenneth

Kljavin, Ivar Roy,Margaret Napier, Mary

Sequence 42, Application US/09944907 Publication No. US20020198147A1

Baker, Kevin

Botstein, David

-09-944-907-42

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; TYPE: PRT ; ORGANISM: Homo Sapien US-09-944-944-42

SEQ ID NO 42 LENGTH: 243

NUMBER OF SEQ ID

NOS:

PRIOR APPLICATION NUMBER: PCT/US01/06520 PRIOR FILING DATE: February 28, 2001

APPLICATION NUMBER: PCT/US00/14042
FILING DATE: May 22, 2000
APPLICATION NUMBER: PCT/US00/20710
FILING DATE: July 28, 2000
APPLICATION NUMBER: PCT/US00/32678
FILING DATE: December 1, 2000

PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000 PRIOR APPLICATION NUMBER: PCT/US00/03565 PRIOR FILING DATE: February 11, 2000

APPLICATION NUMBER: PCT/US00/05841
FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/US00/08439
FILING DATE: March 30, 2000

PRIOR FILING DATE: December

APPLICATION NUMBER: PCT/US99/28301
FILING DATE: December1, 1999
APPLICATION NUMBER: PCT/US99/20095

APPLICATION NUMBER: FILING DATE: NO. US2

US20020173463A1ember PCT/US99/28313

30, 1999

Best Local Similarity 100.0%; Matches 243; Conservative (

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Gaps

Score 243; DB 9; Pred. No. 7.9e-202; Mismatches

Length 243;

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CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 05/049911
PRIOR APPLICATION NUMBER: 60/049911
PRIOR ELING DATE: 1997-06-18
PRIOR ELING DATE: 1997-08-26
PRIOR EPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/05917
PRIOR APPLICATION NUMBER: 60/05917
PRIOR APPLICATION NUMBER: 60/05912
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PRIOR APPLICATION NUMBER: 60/059184
PRIOR APPLICATION NUMBER: 60/059263
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US-10-028-072-362
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US-09-944-929-42
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Matches 243; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VFA 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith, Victoria
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    NUMBER: 60/059588
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Pred. No. 7.9e-202;
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                                                     OR APPLICATION NUMBER: 60/072320
OR FILING DATE: 1998-01-23
OR APPLICATION NUMBER: 60/073612
OR FILING DATE: 1998-02-04
OR APPLICATION NUMBER: 60/074086
OR FILING DATE: 1998-02-09
OR APPLICATION NUMBER: 60/074092
OR FILING DATE: 1998-02-09
OR FILING DATE: 1998-02-09
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A FILING DATE: 1997-10-27

OR APPLICATION NUMBER: 60/063329

OR FILING DATE: 1997-10-27

OR APPLICATION NUMBER: 60/063550

OR FILING DATE: 1997-10-28

OR APPLICATION NUMBER: 60/063561

OR FILING DATE: 1997-10-28

OR APPLICATION NUMBER: 60/06361

OR FILING DATE: 1997-10-28

OR APPLICATION NUMBER: 60/063704

OR FILING DATE: 1997-10-29

OR FILING DATE: 1997-10-29
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OR APPLICATION NUMBER: 60/062814
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/062816
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063045
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063082
OR FILING DATE: 1997-10-30
OR APPLICATION NUMBER: 60/063082
OR FILING DATE: 1997-10-31
OR FILING DATE: 1997-10-31
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FILING DATE: 1998-03-12
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RAPPLICATION NUMBER: 60/059836

OR FILING DATE: 1997-09-24

OR APPLICATION NUMBER: 60/062250

OR FILING DATE: 1997-10-17

OR APPLICATION NUMBER: 60/062285

OR FILING DATE: 1997-10-17
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FILING DATE: 1997-11-17
APPLICATION NUMBER: 60/066364
FILING DATE: 1997-11-21
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FILING DATE: 1997-11-24
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FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063735
FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063738
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FILING DATE: 1997-10-17
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FILING DATE: 1997-10-24
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60/078910
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R FILING DATE: 1998-06
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                           APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-23
                                                                                              APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18
                                                                                                                                                                               APPLICATION NUMBER: 60/088858
FILING DATE: 19/98-06-11
APPLICATION NUMBER: 60/089532
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APPLICATION NUMBER: 60/088730
TO DATE: 1998-06-10
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                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/088026
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FILING DATE: 1998-05-28
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FILING DATE: 1998-04-14
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PELICATION NUMBER: 60/085323
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LENGTH: 243
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
                                                                                                                       TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C17
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APPLICANT:
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                                                                                           CURRENT APPLICATION NUMBER: US/10/121,049 CURRENT FILING DATE: 2002-04-12
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Best Local
                                                                   NUMBER OF SEQ
                           TYPE: PRT
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                                                                               Prior Application
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243; Conserv
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|VFA 243
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Godowski, Paul J.
Gurney, Austin L.
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DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
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                                                                                                                                                                             Watanabe,Colin K
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Smith, Victoria
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o. US20030022239A1
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                                                                           See File Wrapper or Palm
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Pred. No. 7.9e-202;
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APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: APPLICANT: Zhang, Zemin
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC54
CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
PIOT APPLICATION EMBOVED - See File Wrapper or Palm
US-10 NO 362
ENGREY OF SEQ ID NOS: 550
SEQ ID NO 362
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Saplen
                                                                                                                                                          Query Match
Best Local Similarity
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Matches 243; Conservative
   121 APLPEDRVLVNEQGHYDAVTGKETCQVPGVYYFAVHATVYRASLQEDLVKNGESIASEFQ 180
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Godowski, Paul J.
Gurney, Austin L.
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0. US20030022328A1
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; ORGANISM: Homo Sapien
US-10-140-470-362
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CURRENT FILING DAME: 2002-05-06
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
SEQ ID NO 362
LENGTH: 243
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Publication No.
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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Godowski, Paul J.
Gurney, Austin L.
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Wood, William
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GENERAL INFORMATION

FILE REFERENCE:

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; ORGANISM: Homo sapiens
US-09-796-753-68
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PRIOR APPLICATION NUMBER: 09/183,175
PRIOR EILING DATE: 1998-10-30
PRIOR EILING DATE: 1998-12-30
PRIOR EILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR APPLICATION NUMBER: 09/223,546
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PRIOR APPLICATION NUMBER: 09/223,546
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R FILING DATE: 2000-00
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APPLICATION
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              1 MRPLLVLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG 60
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                                                                 Conservative
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IVENTION: SECRETED PROTEINS AND USES THEREOF

SMCE: 7853-227-999
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US-10-175-746-362
US-10-nce 362, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
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               181 FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
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FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
                                                  61 APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
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Gurney, Austin L.
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p. US20030027270A1
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SEQ ID NO 68 LENGTH: 243 TYPE: PRT

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RESULT 13 US-10-176-918-362

GENERAL INFORMATION

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P339ARL(382
CURRENT APPLICATION NUMBER: US/10/176,918
CURRENT FILING DATE: 2002-06-20
PILOT APPLICATION TEMOVED - See FILE Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 362
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-918-362
                                     Sequence 362, Application US/10176921 Publication No. US20030027276A1 GENERAL INFORMATION:
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SEQ ID NO 362
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-921-362
                                                                                                                                                                                                  Sequence 362, Application US/10137865 Publication No. US20030032155A1 GENERAL INFORMATION:
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DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
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                                   Sherwood, Steven Smith, Victoria
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Godowski, Paul J.
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ORGANISM: Homo Sapien
US-10-137-865-362
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## ALIGNMENTS

AUTHORS	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX464228	
Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E., Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1	Homo sapiens	human.		AX464228.1 GI:21899130	AX464228	361 from Patent W00140466	AX464228 1377 bp DNA		

APPROXICE OF A

Pred. No.

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BASE COUNT ORIGIN

Query Match Best Local Matches

FEATURES Source

TITLE JOURNAL

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CCAGGTGCCTGGGGTCTACTACTTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCA
                 GCCCAAGCCAGCCTCGCTCTCGGGGGGGGGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGT
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/db_xref="taxon:9606"
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                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Sh
TOShiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Center, Stanford University School of Medicine, Stanford, CA
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and My
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This clone was selected for full length sequencing because it
                                                                                                                                                                                                Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                     Homo sapiens, C1q and tumor necrosis factor related clone MGC:32938 IMAGE:5278184, mRNA, complete cds BC029485
BC029485.1 GI:20810468
MGC.
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1 (bases 1 to 1370)
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PRI 16-MAY-2002 protein 5,

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614 CGTGCTGGTGAACGAGGACATTACGACGCCGTCACCGGCAAGTTCACCTGCCAGGT 673 667 GCCTGGGGTCTACTTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGA 726	7	547 CGCCAAGCGCTCCGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCTTGCCCCTTCGACCG 606 .			GGGGGGAGGCGGGGGCGGGGGGGGGGGGGGGGGGGGGG	367 GGGCCGCGATGGCCGCGACGGCGCGCGACGGCGCCCGGGGGCTCCGGGAGAGAAAGGCGA 426				194 GCGAGAGGACCCCGGCGTCCGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCCTCCT 246	87	127 GGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGGACT 186	74 GACGCCAGGGGGGCCCTGGCCGGGAGAAGCGCGGGGCTGGAGCACCACCACCT 126 74 GACGCCAGGGAGCAGCAGCCTGGCCGGGGAGAAAGCGCGGGGCTGGAGCACCACCAACT 133		TTCTCTTGGAGTCTGGGAGGAAGGAAAGCGGAGCCGACCGA	97.98; Similarity 99.68;	239 а	RSAFSAKRSESRVPPPSDAPLPFDRVLVNRQGHYDAVGKRTTQVPGVYYFAVHATVY RASLQFDLVKNGESIASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIY ASTFTRSTESCETTVCCTTTTG	/translation="MRPLIVILLIGIAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSR GLPGRDGRDGAPGAPGREGEGRPGLPGPRGPPGFACEACEACEACEACEACEACEACEACEACEACEACEACEA	<pre>/product=*Clq and tumor necrosis factor related protein 5" /protein_id="AAH29485.1" /db xref="dr-70810468".</pre>			/Lissue_type="Brain, hypothalamus" /Clone_lib="NIH MGC 96"	:114902"	Source 1. 1370 /organism="Homo sapiens"	passed the following selection criteria: matched mRNA gl: 14149711.
FEATURES SOURCE	TITLE Dire		REFERENCE 1 ( AUTHORS Shep TITLE Homo	ž	RDS	ž	RESULT 3 AF329841 LOCUS	Db 1334 To	Оу 1327 т	1274	Ov 1267 T	1207	Db 1154 T	1094	QV 1087 T	1027	Db 974 (	914	ФУ 907 (	Db 854	Оу 847	794	787		Db 674	
USA		Unpublished Companies of Callette Protein Recrosts Factor-related protein Protein Recrost Factor-related Pr	Catarrhini; H	Cranjata: Vertebrata.	AF329841.1 GI:13274527	Homo sapiens complement-clq tumor necrosis factor-related protein (CTRP5) mRNA, complete cds.		TCAATAAACCTAAGAACCCTCAAAAAAAAAAAAAAA 1370	1363	THE TEST OF THE PROPERTY OF TH	ICCCACACTTGCTCTGGTCCAGGAGCCCACGGTGGGGTGCTCTCTTCCTGGTCCTCTGC 1273		TGGGGCAGTGGCTGGATTTCTGCCCAAGACCAGAGGAGTGTGCTGTGCTGGCAAGTGTAA 1206 	TCCGTCCTGCTGCCAAGGAATGGGAACAGTGGCTGTCTGCGATCAGGTCTGGCAGCA 1146 TCCGTCCTGCTGCCAAGGAATGGGAACAGTGGCTGTCTGCGATCAGGTCTGGCAGCA 1153	CAGGAGGGCTGGCCCTCCTGGAATATTGTGAATGACTAGGGAGGTGGGGTAGAGCACTC 1093		CAPAGE TO ACCITCATECTICITACING TO ACAGAGGAGGTTGAGGCTGACAACCAGGTCAT 1026	CTCCGGATTTCTGGTGTACTCCGACTGGCACAGCTCCCCAGTCTTTGCTTAGTGCCCACT 973		GCAGGTGGGTGTGGCTACATTGGCATCTATGCCAGCATCAAGACAGCACCTT 913		4 1	TUTUUFGAAGAATGGCGAATCCATTGCCTCTTTCTTCCAGTTTTTCGGGGGGGTGGCCCAA 793		GCCTGGGGTCTACTACTTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGA 733	

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                 GGACCCCGGGCCGCGAGGAGAGGCGGGACCCGCGGGGCCCACCGGGCCTGCCGGGAGTG
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/product="complement-clq tumor
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AGGAGTGTGCTGCTGCCAGGTGTAAGTCCCCCCAGTTGCTCTGGTCCAGGAGCCCCACGG 1239
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                                                          PolyA_signal
PolyA_site
BASE COUNT 18;
ORIGIN
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HSM800923
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  Query Match
Best Local Similarity 99:
Matches 1065; Conservative
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de; sequenced by MediGenomix (Martinsried/German) within the cDNA (DKF2p586B0621) is available at the RZPD in Berlin. Please contained the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://www.mips.biochem.mpg.de/proj/cDNA/.
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AL110261
AL110261.1 G
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Submitted (15-AUG-1999) MIPS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1068)
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DHLOB; sites Not! + Sali/Miu!"
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RPFLANGGGAMVRLEPEDQVMVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSPVF
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1049
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<1. .660
                                                                                                                                                                                                             /note="similarity to complement subcomponent
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     0;
Score 1064.4; DB 9;
Pred. No. 9.2e-174;
0; Mismatches 1;
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DKFZp586B0621 (from
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Best Local Similarity
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Submisted (12 MAR-2001) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Cancer Center Research Institute
Cancer Genomic Division
5-1-1, Tsukiji, Chuo-ku, Tokyo, Japan
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AP003396
AP003396.1 G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yarai@ncc.go.jp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hor Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Homo sapiens genomic DNA Published Only in Database (2002)

2 (bases 1 to 191362)

Hattori M. Tohii W. Toroda N. Toroda N. Tohia W. Tohia W. Toroda N. Toroda N. Tohia W. Toroda N. Toroda 
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/clone="RP11-334E6"
45977 c 48722 g
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genomic DNA, chromosome
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Pred. No. 2.6e-147;
0; Mismatches 2;
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Catarrhini;
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1; Hominidae; Homo
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DNA, chromosome 11q clone:R1105h09, complete
         GDB:198117, stSG29284, stSG50535, A002048, stS
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non-AGCT bases: none
Additional author info
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National Cancer Center Research
                                    GCTGGCAAGGAATGGGAACAGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTGG
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                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                               Web site: http://hgp.gsc.riken.go.jp/
Contact: hattorl@gsc.riken.go.jp
Contact: hattorl@gsc.riken.go.jp
Contact: hattorl@gsc.riken.go.jp
Center project Information
Center project name: Humbraftl1
Center clone name: RP11-680A7
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Chemistry: Program: Phrap; version 0.990329
Consensus quality: 17559 bases at least 040
Consensus quality: 17555 bases at least 030
Consensus quality: 179768 bases at least 030
Consensus quality: 179768 bases at least 020
Quality coverage: 9.01x in 020 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (29-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, On Nov 3, 2000 this sequence version replaced gi:8117391.

Center: RIKEN.Genomic Sciences Center(GSC)
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1 (bases 1 to 182429)

Hattori, Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,

Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Published Only in DataBase (2000)

2 (bases 1 to 182429)

Lattori M. Taylor, T.D., Hong-Seog, P.,

Published Only in DataBase (2000)
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                                                                                                                                  178309 178408: gap of
178409 180918: cont
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35 136903; contig of 8669 bp in 16

104 137003; gap of 100 bp

104 145887; contig of 8884 bp in 17

388 145987; gap of 100 bp

988 153199; contig of 7212 bp in 1
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                                                                                                1018: gap of 182429: contig of
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178308: contig of 2603
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                                                          ACTACTTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGA 737
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Pred. No. 5.8e-145;
0; Mismatches 3;
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                                                                               Kameya,S., Naggert,J.K. and Nishina,P.M. Direct Submission Submitted (17-JAN-2002) The Jackson Labo
                                                                                                                                  Mfrp, a gene encoding a frizzled related protein, mouse retinal degeneration 6 Hum. Mol. Genet. 11 (16), 1879-1886 (2002)
                                                                                                                                                                                                                                                                                             AF469650

4220 bp mRNA linear ROD 31-JUL-2002 mus musculus membrane-type frizzled-related protein (Mfrp) and complement-clq tumor necrosis factor-related protein (Clqtnf5)
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AF469650
                                                                                                                                                                                                                                               Mus musculus.
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Query Match Best Local Sim. Matches 909;

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Sequence updated (26-May-2000).

**NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
On May 31, 2000 this sequence
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           1 1558: contig of 1558 bp
1559 1568: gap of 100 bp
15659 33689: contig of 18031 bp
33690 33789: gap of 100 bp
47432: contig of 13643 bp
47433 47532: gap of 100 bp
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Contact: hattor1@gsc.riken.go.jp
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166758. .168307
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                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.g. Series: IRAK Plate: 61 Row: f Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                       analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert:
                                                                                                                                                                                                                                                                                                                                   Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S. Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (05-MAR-2002) National Institutes of Health, Mammallan Sene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing Center
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                                                                                             /tissue_type="Mammary tumor. Meta
model. 10 month old virgin mouse.
/clone_lib="NCI_CGAP_Mam1"
/codon_start=1
/product="Unknown (protein for MGC:36714)"
/protein_id="AAH25174.1"
/db_xref="GI:19263584"
                                                                                     /lab_host="DH10B"
                                                                    /note="Vector: pCMV-SPORT6"
                                                                                                                                            /clone="MGC:36714 IMAGE:3978387"
                                                                                                                                                             /map="FVB/N"
                                                                                                                                                                       /organism="Mus musculus"
/db_xref="taxon:10090"
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Rus musculus
Eukaryota; Metazoa; Ch
Manumalia; Eutheria; Rc
Manumalia; 1 to 1271)
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                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLML at: http://image.lln Series: IRAK Plate: 54 Row: b Column: 4
This clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus, Similar to DKFZP586B0621 protein, IMAGE:5355789, mRNA, complete cds. BC023068 BC023068.1 GI:18606999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Baylor College of Medicine Human
                                                                                                                                                                                                                                                                      analysis
                                                                                                                                                                                                                                                                                                                                                                                                       Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., I
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G.,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (04-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing Center
Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: MGC help desk
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ductal carcinoma. 5 month old v
/clone_lib="NCI_CGAP_Mam6"
/lab_host="DH10B"
/note="Vector: pcMV-SPORT6"
153. .884
                                                                                                                                        /map="FVB/N"
/clone="MGC:38635 IMAGE:5355789"
                                                                                                                                                                                                                                                Location/Qualifiers
/codon_start=1
                                                                                                                                                                                    /db_xref="taxon:10090"
                                                                                                                                                                                                        /organism="Mus musculus"
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Rodentia;
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       AGGAGGGCTGGCCCCCCTGGAATATTGTGAATGACTAGGGAGGTGGGGTAGAGCACTCTC 1088
                                       AAAGTGAGCTCATGCTCTCACTCCTAGAAGGAGGGTGTGAGGCTGACAACCAGGTCATCC
                                                         CCGGATTTCTGGTGTACTCCGACTGGCACAGCTCCCCAGTCTTTTGCTTAGTGCCCACTGC 968
                                                                                           CAGCCTCGCTCTCGGGGGGGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGC
                                                                                                                                                              ACCCGGAGCTGGCACTTGCTCCTCAGTGGAGGGTGTGACACTAACCCGCGCAGCGCATAC
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/protein_id="AAH23068.1"
/db_xref="G1:18605994"
50.2%;
77.9%;
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NOTE: This is a 'working draft' sequence. It currently consists of 42 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-FEB-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://ngp.gsc.riken.go.jp/, Tel:81-42-778-9923, Eax:81-42-778-9924)
On May 31, 2000 this sequence version replaced q1:6997842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Homo sapiens 198, 902 genomic DNA of 11q23
Published Only in DataBase (2000)
2 (bases 1 to 198902)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y., Suhittori, M., Taylor, T.D., Totoki, Y., Watanabe, H. and Sakaki, Y., Suhittori, M., Taylor, T., Watanabe, H. and Sakaki, Y., Suhittori, M., Taylor, T., Watanabe, H. and Sakaki, Y., Suhittori, M., Taylor, T., Watanabe, H. and Sakaki, Y., Suhittori, M., Taylor, T., Watanabe, H. and Sakaki, Y., Suhittori, M., Taylor, T., Watanabe, H. and Sakaki, Y., Suhittori, M., Taylor, T., Toyoda, A., Taylor, T., Watanabe, H. and Sakaki, Y., Suhittori, M., Taylor, T., Watanabe, H. and Sakaki, Y., Suhittori, M., Taylor, T., Watanabe, H. and Sakaki, Y., Suhittori, M., Taylor, T., Watanabe, H. and Sakaki, Y., Suhittori, M., Taylor, T., Watanabe, H. and Sakaki, Y., Suhittori, M., Taylor, T., Watanabe, H. and Sakaki, Y., Suhittori, M., Taylor, T., Watanabe, H. and Sakaki, Y., Suhittori, M., Taylor, T., Watanabe, H. and Sakaki, Y., Suhittori, M., Taylor, T., Watanabe, H. and Sakaki, Y., Suhittori, M., Taylor, T., Watanabe, H. and Sakaki, Y., Suhittori, M., Suhi
                                                                                                                                                                                Sequencing vector: PCR products; 100% of reads
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of re
Assembly program: Phrap; version 0.990329
Consensus quality: 171788 bases at least 040
Consensus quality: 19184443 bases at least 030
Consensus quality: 191295 bases at least 020
Insert size: 194802; sum-of-contigs
Quality coverage: 4.12x in Q20 bases; sum-of-cont
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Center clone name: RP11-657A24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattoriegsc.riken.go.jp
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sapiens DNA, clone:RP11-657A24.
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74070: gap of 8107: contig o 81107: gap of 87320: contig o 87420: gap of 87420: gap of 93250: contig o	100 bp in 100 bp	195658 contig of 1270 bp in leng 19707 contig of 1949 bp in leng 19802 contig of 1955 bp in leng polated (26-May-2000).  Is 1s a 'working draft' sequence. It of 42 contigs. The true order of the lown and their order in this sequence own and their order in this sequence ', Gaps between the contigs are represely, but the exact sizes of the gaps are ord will be updated with the finished is it is available and the accession not contiged.	169851 contig of 3630 bp in 172048 contig of 2097 bp in 17332 contig of 3184 bp in 17934 contig of 2482 bp in 179975 contig of 1861 bp in 181604 contig of 1629 bp in 183951 contig of 2247 bp in 185927 contig of 1876 bp in 187870 contig of 1876 bp in 187870 contig of 1873 bp in 187870 contig of 1843 bp in 187870 contig of 1843 bp in 187870 contig of 1621 bp in 192527 contig of 1621 bp in 192527 contig of 1661 bp in 194288 contig of 1661 bp in	contig of 4876 bp in contig of 4876 bp in contig of 5976 bp in contig of 5976 bp in contig of 5292 bp in contig of 5292 bp in contig of 5425 bp in contig of 5607 bp in contig of 5012 bp in contig of 3342 bp in contig of 3796 bp in contig of 3796 bp in contig of 4438 bp in contig of 4438 bp in contig of 4438 bp in contig of 4082 bp in contig of	it is available and the accession nu  20627 contig of 20627 bp in len 31817 contig of 11090 bp in len 41131 contig of 9214 bp in len 49745 contig of 8514 bp in len 59457 contig of 9612 bp in len 66804 contig of 7247 bp in len 66804 contig of 7247 bp in len 73970 contig of 7066 bp in len 73970 contig of 6937 bp in len 87320 contig of 6213 bp in len 87320 contig of 6213 bp in len 97365 contig of 5830 bp in len 97365 contig of 5830 bp in len 97365 contig of 6830 bp in len
/organism-"Homo sapiens" /db_xref="taxon:9606" /chromosome="11" /chromosome="11" /map="1123" /clone="RP11-657A24" /note="assembly_fragment"	191299; gap of 100 bp 192527; contig of 1258 bp 192627; gap of 100 bp 194288; contig of 1661 bp 194388; gap of 100 bp 19558; gap of 1270 bp 195707; contig of 1949 bp 197807; gap of 100 bp 197807; gap of 100 bp 198902; contig of 1095 bp cation/qualifiers	5 179875; contig of 1861 bp in 17975; gap of 100 bp 181604; contig of 1629 bp in 181704; gap of 100 bp 100	158821: gap of 100 bp 1126203: contig of 4082 bp in 163003: gap of 100 bp 116221: gap of 110 bp 116222: gap of 100 bp 116221: gap of 100 bp 1172448: gap of 100 bp 1175432: contig of 2097 bp in 175432: gap of 100 bp 175632: gap of 100 bp 17563	129766: contig of 5425 bp in 29866: gap of 100 bp in 35573: gap of 1607 bp in 35573: gap of 5012 bp in 16085: gap of 100 bp in 16085: gap of 100 bp in 164027: contig of 3342 bp in 164027: contig of 3342 bp in 16023: gap of 100 bp in 16023: gap of 100 bp in 152461: contig of 4388 bp in 155444: gap of 100 bp in 155441: gap of 100 bp in 155441: gap of 100 bp in 155471: contig of 4377 bp in 1	1 93350: gap of 97965: contig of 98065: gap of 102941: contig of 103041: gap of 103117: contig of 109117: gap of 113391: contig of 113491: gap of 118883: gap of 118883: gap of

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Best Local Similarity
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                                                                                              173657 bp
Rattin norvegicus clone CH230-904,
72 unordered pieces.
AC112557
AC112557.2 GI:21735369
HTG: HTGS_PHASE1.
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Alsbrooks,S.L., Amaratunge,H.C., A
Barbarla,J., Benton,J., Bimage,K.,
                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                               Rattus norvegicus
                                                   Rattus
                                                                                             Norway rat.
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                                                                                                                                                                                                                                                                                              ATCCTCCCCACCCCCCTCCTGCTGCTGGGGCCGGCCCTTTTCTCAGAGATCACTCAATAAA 1334
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41232. .49745
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31918. .41131
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99.7%; Pred. No. 3.1
                                                         Chordata;
Rodentia;
          Adio-Oduola, B., Ali-osman, F.R., tunge, H.C., Are, J.R., Ayele, M., 1
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                                                     Craniata; Vertebrata; I
Sciurognathi; Muridae;
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re,J.R., Ayele,M., Banks,T.,
Blankenburg,K., Bonnin,D.,
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Balay, C., Bovido, S., Bristow, M., Brown, R., Bryant, N.P.,
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43135: Gontig of 1357 bp 1 4325: gap of unknown leng 45193: contig of 1938 bp i 45293: gap of unknown leng 47217: contig of 1924 bp i 47317: gap of unknown leng 47317: gap of unknown leng 49331: gap of unknown leng	33128: contig of 1478 33228: gap of unknown 34763: contig of 1535 34863: gap of unknown 36404: contig of 1541 36504: gap of unknown 37957: contig of 1453 48057: gap of unknown 40293: contig of 2236 40393: gap of unknown 41698: contig of 1305 41798: gap of unknown	24684: contig of 1738 24784: gap of unknown 26405: contig of 1621 26505: gap of unknown 27716: contig of 1211 27816: gap of unknown 2876: contig of 1060 28976: gap of unknown 30019: contig of 1043 30119: gap of unknown 31550: contig of 1043 31550: contig of 1043	gap of unknown leg- contig of 1127 bp gap of unknown leg- contig of 1053 bp gap of unknown leg- contig of 1674 bp gap of unknown leg- contig of 1077 bp gap of unknown leg- contig of 1156 bp gap of unknown leg- contig of 1156 bp gap of unknown leg- contig of 1158 bp gap of unknown leg- contig of 1151 bp gap of unknown leg- contig of 1103 bp gap of unknown leg- contig of 1103 bp	1137: contig of 1137 bp in 1237: gap of unknown length 2720: contig of 1483 bp in 2820: gap of unknown length 3984: contig of 1164 bp in 4084: gap of unknown length 5258: gap of unknown length 5258: gap of unknown length 6306: contig of 1018 bp in 6406: gap of unknown length 7523: contig of 1019 bp in 7623: gap of unknown length 8631: contig of 1008 bp in 8731: gap of unknown length 8731: gap of unknown length 9806: contig of 1075 bp in 8731: gap of unknown length 11255: contig of 1249 bp in 11255: gap of unknown length 112568: contig of 1313 bp in 12568: gap of unknown length 12568: contig of 1313 bp in 12568: gap of unknown length 12568: contig of 1313 bp in 12568	arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
OY  738 ATGGCAATCCATTGCCTCTTTCTCCAGTTTTTCGGGGGGTGGCCCAAGCCAGCC	558 CGGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCTTCGACCGCGTGCTGATGA	3 2; 9; 71; GAGG 1     GTGG GATC	83551 836053 86053 86153 86153 88659 98759 99078 90178 92201 92301 94277 94977 94977 96946 97046	unknown lengtl of 2325 bp in unknown lengtl of 1809 bp in unknown lengtl of 300 bp in of 300 bp in of 1767 bp in of 1767 bp in unknown lengtl of 2158 bp in unknown lengtl of 2779 bp in unknown length of 2779 bp in unknown length of 2794 bp in unknown length of 2795 bp in unknown length of 3457 bp in inknown length of 1900 bp in inknown length of 3457 bp in inknown length of 3457 bp in	5120 5130 5311

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181 GCNCCNGGNGARAARGGNGARGGNGANGCCCAGCCAGCCAGCCMGNCCNGGNGATTACCAGGAGTAGAGAGAGAGAGAGAGAGAGAGAGAGA	DЪ	Qy	Db	Qγ	Db	Qy	Db	Qy	DЬ	Qy	Db	Ϋ́	) Db	Qy	) Db	Ş	)	. 5	Db .
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Search completed: June 22, 2003, 04:43:30 Job time: 3606 secs

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Human colon cancer
Murine TANGO 253 c
Murine secreted pr
Murine secret

cDNA encoding rat Skin cell cDNA, SE Rat cDNA isolated

TATE OF STREET

Human secreted pro
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CDNA encoding rat
Skin cell cDNA, SE
Rat CDNA isolated
cDNA encoding rat
Skin cell cDNA, SE
Rat CDNA isolated

cDNA sequence #15 Human TANGO 253 OR Human secreted DNA encoding no

novel e #15

Human

pro

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Botstein

660

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This is the nucleotide sequence of cDNA clone DNA40592 (ATCC 209492)
C codding for human PRO344 (UNQ303) (see AAX06481). The clone was
codding for human PRO344 (UNQ303) (see AAX06481). The clone was
closed the discontinuous formation of DNA40592
C was observed in primary lung tumours and in primary colon tumours,
C was observed in primary lung tumours and in primary colon tumours,
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C cutility in cancer therapy. The invention identifies 14 genes (see
C cutility in cancer therapy. The invention of tumour cells. Such
c cutility in cancer therapy. The invention of tumour cells. Such
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c cutility in cancer therapy. The invention of tumour cells. Such
c cutility in cancer therapy. The invention of tumour cells. Such
c camplification is expected to be associated with overexpression of
c the gene product and to constribute to tumorigenesis. The encoded
c and/or treatment (including prevention) of certain cancers, and may
c act as predictors of the prognosis of tumour treatment.
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P-PSDB; AAY06481.
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10-NOV-1998;
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98US-0107783.
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Pred. No. 1.7e-244;
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                                             Human; PRO protein; tumour necrosis factor family; TNI secreted protein; transmembrane protein; inflammation
                                                                                  Human PRO344 nucleotide sequence
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                                                                                                                                                                                                                                              The present invention describes nucleic acids encoding PRO secreted and transmembrane proteins used therapeutically. The PRO proteins have cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy, identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses.
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05-JAN-1998;
09-FEB-1998;
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 CAGCCTCTGCCCGGGGCACCCCGGGCTTCCAGGCACGCCGGGCCACCATGGCAGCGAGGG
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tive 0; Mismatches
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Query Match
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                                                                                                                                        The present sequence is the cDNA clone, designated as DNA40592-1242, encoding the human PRO344 polypeptide. It is isolated from human foetal lung tissue cDNA library, identified using probes based on a consensus sequence DNA34398, derived from secreted protein extracellular domain NC: 209422. PRO344 functions as a neoplastic cell growth inhibitor and and PRO344. This compositions as a neoplastic cell growth inhibitor and and PRO344. This composition is especially useful for treatment of human cancers such as breast, prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.
                                                                                                                                                                                                                                                                                                                                           01-DEC-1998;
16-DEC-1998;
22-DEC-1998;
20-JUL-1999;
26-JUL-1999;
                                                                                                                        Sequence 1377 BP; 251 A;
                                                                                                                                                                                                                                    Claim
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                                                 GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAGCCGGAGCCGGCAGGGAGCGAACCAGGAC
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Pred. No. 1.7e-244;
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                    The present sequence encodes a novel human polypeptide. The specification describes novel polypeptides designated PRO201, PRO292, PRO327, PRO1265, PRO314, PRO343, PRO347, PRO357, PRO715, PRO1017, PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumourigenesis. The polypeptides are useful target for the identification of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies against these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth
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01-DEC-1999;
02-DEC-1999;
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08-MAR-1999;

02-JUN-1999;

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                                                                                                           Claim 50; Fig
                                                                                                                        New anti-polypeptide antibody useful in neoplastic cell growth and proliferation
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PRO715;
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P-PSDB; AAY93688.
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Hillan KJ,
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16-DEC-1998;
22-DEC-1998;
      Claim
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                                                                                                                                         01-DEC-1999;
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                                                                                                                                                                                                                                    PRO: membrane bound protein; secreted protein; PRO357; PRO327; PRO243; PRO715; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347; PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide; antibody; screening; detection; inhibition; probe; primer; human;
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                  human nucleic acids of ypeptides, designated diagnostic agents
                                               2000-412324/35.
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ME, Goddard A
Kljavin IJ,
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                                                                                                           98WO-US25108.
98US-0112850.
98US-0113296.
                                                                                                                                       99WO-US28301
   187pp; English
                                                                                                                                                                                       Location/Qualifiers
227..958
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d as PRO p
                                                               Eaton DL, Ferrara N, Filvaroff E;
A, Godowski PJ, Grimaldi CJ, Gurney
Napler MA, Roy MA, Tumas D, Wood W
                                                                                                                                                                                PRO344 polypeptide
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                        g secreted and
polypeptides,
                    transmembrane
useful as pharmaceutical
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Best Local S
Matches 1377
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mes 1377; Conserv
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GCCCAAGCCAGCCTCGCTCTCGGGGGGGGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGT
                                                               CCAGGTGCCTGGGGTCTACTACTTCGCCGTCCATGCCACCGTCTACCGGGGCCAGCCTGCA
                                                                                                                                       CGACCGCGTGCTGGTGAACGAGCAGGGACATTACGACGCCGTCACCGGCAAGTTCACCTG
                                                                                                                                                                          CTTCAGCGCCAAGCGCTCCGAGAGCCGGGTGCCTCCGGCCGTCTGACGCACCCTTGCCCTT
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ilarity 100.0%;
Conservative (
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Pred. No. 1.7e-244;
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L, Filvaroff E, y AL, Sherwood WI, Zhang

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Zhang

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RESULT 6
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03-DEC-1999;
16-DEC-1999;
20-DEC-1999;
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20-DEC-1999;
30-DEC-1999;
30-DE
                                                                                                                                                                                                                                                                                                                                                                                                                           Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal mu; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
                                                                                                                                                                                                                                                                                                         01-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA sequence encoding for PRO344 polypeptide.
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99WO-US28531
99WO-US28554
99WO-US28564
99WO-US28564
99WO-US28565
99WO-US3099
99WO-US30991
99WO-US30124
2000WO-US00277
2000WO-US00276
2000WO-US03124
2000WO-US03124
2000WO-US03124
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                                                                                                                                                                                                                                                                                                                                                                                                  ASS21244-AAS21518 encode for novel human secretory and transmembrane CC PRO polypeptides. The PRO polypeptides are useful to detect other CC PRO polypeptides, to modulate biological activities of cells expressing CC PRO polypeptides, and to detect the presence of mammalian lung, colon, propertide expression in a cell sample to that in a control sample. CC come of the 275 sequences are also useful to stimulate the release of color, polypeptide expression in a cell sample to that in a control sample. CC tumour necrosis factor-alpha (PNF-alpha) from human blood, the CC gene expression in pericyte cells, the release of proliferation or differentiation of chondrocytes, the proliferation or cc cartilage, the proliferation of inner ear utricular supporting cells or CC cartilage, the proliferation of inner ear utricular supporting cells or confocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by consecute involved in binding interactions. The polynucleotides encoding CC molecules involved in binding interactions. The polynucleotides encoding cransgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 1377; Conserv
                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Gerritsen
Smith V,
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24-FEB-2000;
24-FEB-2000;
24-FEB-2000;
01-MAR-2000;
20-MAR-2000;
21-MAR-2000;
30-MAR-2000;
17-MAY-2000;
22-MAY-2000;
30-MAY-2000;
10-NOV-2000;
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DB; AAU12352.
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CGTCCTGCTGCTCCTGGGGCCTGGCGGCCTCGCCCCCACTGGACGACAACAAGATCCC
                                                                                                                                                                   TGGGGTGACGGCAGGCAGGGGGGGGGGGCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCA
                                GACTAGTTCTCTTGGAGTCTGGGAGGAGGAGGAAGCGGAGCCGGCAGGGAGCGAACCAGGAC
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Stewart TA,
                                                                                                                                                                                                                                                                                                                100.0%; Score 1377; DB 22; ilarity 100.0%; Pred. No. 1.7e-244; Conservative 0; Mismatches 0; 1
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                                                                                                                                                                                                                                                                                                                                                                            BP; 251 A; 422 C; 472 G; 232 T; 0 other;
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A, Godowski PJ, Gurney I
Tumas D, Watanabe CK, Wc
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Indels

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Gaps

240 240 180 180 120 120 60

APPROPRIEST CONTRACTOR OF THE CO.

Length 1377;

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29-JAN-2001 (first entry)
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                           CDNA;
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KW Human; immune related disease; diagnosis; antlinflammatory; cardiant; KW dermatological; antlithyroid; antlitheumatic; immunosuppressive; hemotosistic; antlithyroid; antlidiabetic; nootropic; neuroprotective; antlianaemic; hepatotropic; virucide; antipsoriatic; antiallergic; virucide; antipsoriatic; antiallergic; virucide; antipsoriatic; antiallergic; virucide; antipsoriatic; spread of the virucide; antipsoriatic; antiallergic; virucide; antipsoriatic; antiallergic; virucide; antipsoriatic; sarcoidosis; virucide; antipsoriatic; sarcoidosis; virucide; viruci

W0200053758-A2

02-MAR-2000; 2000WO-US05841.

14-SEP-2000

GCCCAAGCCAGCCTCGCTCTCGGGGGGGGCCATGCTGAGGCTGGAGCCTGAGGACCAAGT

CCAGGTGCCTGGGGTCTACTACTTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCA

CTTCAGCGCCAAGCGCTCCGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCTTGACCTT

600

540 540 480 480 420 420 360 360 300

660 660

600

Human PRO344 protein UNQ303

encoding cDNA SEQ ID NO:240

AAC58626; AAC58626

960 960

900

900 840 840 780 780 720 720

781 781 721 721 199 661 109 601 541 541 481 481 421 421 361 361 301 301 241

30-NOV-1999 30-NOV-1999 01-DEC-1999 01-DEC-1999 01-DEC-1999 02-DEC-1999 02-DEC-1999 02-DEC-1999 20-DEC-1999 20-DEC-1999 30-DEC-1999 30-DEC-1999 30-DEC-1999 30-DEC-1999 30-DEC-1999 16-JAN-2000 06-JAN-2000 06-JAN-2000 11-FEB-2000 05-OCT-1999; 29-OCT-1999; 29-NOV-1999; 08-SEP-1999; 15-SEP-1999; 28-JUL-1999; 01-SEP-1999; 15-SEP-1999 13-SEP-1999; 20-JUL-1999; 23-MAR-1999 12-MAR-1999, -SEP-1999; 99WO-US31095 99WO-US31099 99WO-US31274 2000WO-US00219 2000WO-US00277 2000WO-US00376 2000WO-US003565 2000WO-US034541 99WO-US28409. 99WO-US28301. 99WO-US28634. 99WO-US28551. 99WO-US28564. 99WO-US28565. 99US-0162506. 99WO-US28214. 99WO-US28313. 990S-0141037 990S-0144758 990S-0146282 990S-0146222 990G-0120111 990G-0120594 990G-0120944 990G-0121090 990G-0121147 99US-0131445. 99US-0132371. 99US-0134287. 99WO-US05028. 99US-0123618. 99US-0123957. 99WO-US12252 99WO-US08615 9905-0128849

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GCACTCTCCGTCCTGCTGCCAGGAATGGGAACAGTGGCTGTCTGCGATCAGGTCTG 1140

CCCACTGCAAAGTGAGCTCATGCTCTCACTCCTAGAAGGAGGGTGTGAGGCTGACAACCA 1020

1260

1200 1200

1081 1081

1021 1021 961 961 901 901

1321

18-FEB-2000; 22-FEB-2000;

Claim

540

480

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The present invention describes sixty four human PRO proteins which can CC be used in the treatment of immune related diseases. The human PRO CC proteins, anti-PRO antibodies, agonists and antagonists are useful for CC treating and diagnosing immune related disorders. The disorders are CC estected from systemic lupus erythematosus, rheumatoid arthritis, luvenile chronic arthritis, spondyloarthropathies, CC systemic scierosis, idiopathic inflammatory myopathies, Sjogren's CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic canaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, CC and peripheral nervous systems, hepatobiliary diseases of the central CC bowel disease, gluten-sensitive enteropathy and Whipple's disease, CC autoimmune or immune-mediated skin diseases, allergic disease, CC diseases including graft rejection and graft-versus-host-disease.

CC AAB33414 to AAB3477 represent PCR primers and hybridisation probes used CC AAB33414 to AAB3477 represent human PRO polynucleotide and protein the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1377 BP; 251 A; 423 C; 471 G; 232 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sixty four PRO polypeptides, useful in the diagnosis and tree immune related disorders, e.g. systemic lupus erythematosis, arthritis, osteoarthritis, thyroiditis and diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                        AGGCGAGGGCGGAGGCCGGGACTCCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGA
                                                                               CTTGCCGGGCGATGGCCGCGACGGCGCGCGCGCGCGGGGCTCCGGGAGAGAA
                                                                                                                             CCAACTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGG
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Query Match Best Local Matches

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CC protein zsig39 (AAW97984). Claimed polynucleotides comprise CC nucleotides 243-962, 252-962, 285-485, 285-485, 285-485, 285-485, 285-485, 285-485, 285-485, 285-485, 285-486, 285-481, 285-491, 491-926 of this isolated polynucleotide. CC 285-491, 285-491, 491-926 of this isolated polynucleotide. CC EST database for secretory signal sequences characterised by an CC 13 amino acids and a cleavage site. A single EST sequence was CC 13 amino acids and the novel polypeptide encoded by the full-length CC discovered, and the novel polypeptide encoded by the full-length CC adipocyte complement related protein Acr930 and adipocyte secreted CC protein appll. A full-length clone was obtained from a lung tissue vectors, cultured cells and a method of producing zsig39 polypeptide care claimed, as well as probes and primers (useful in diagnostic CC entabolism by administering a zsig39 polypeptide. The zsig39 polypeptide cc polypeptide may also be used in organ preservation, for cryopreservation, for surgical pretreatment to prevent injury due cc promoting lysis or phagocytosis of infectious agents.
                                                                                                        Query Match
Best Local Similarity
Matches 1324; Conserv
                                                                                                                                            Sequence 1347
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252.926
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                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences human and murine secreted or transmembrane proteins TANGO 253, TTANGO 281 and INTERCEPT 258. These are useful in the treatment occionary, pulmonary, olfactory, immunological, neurological, developmental and kidney disorders.
                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                             New nucleic acids for treating diseases and disorders, e.g. atherosclerosis, infection, autoimmune diseases, obesity, ear disorders, brain disorders, tumors, diabetes, arthritis, multiple sclerosis and asthma.
                                                                                                                                                                                                                                                                                                                         Claim
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New nucleic acids WPI; 2001-050109/06.

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The present invention provides the protein and coding sequences of human and murine secreted or transmembrane proteins TANGO 253, TANGO 281 and INTERCEPT 258. These are useful in the treatment of coronary, pulmonary, olfactory, immunological, neurological, developmental and kidney disorders.
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TANGO253; TANGO 257; TANGO 281;
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                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences human and murine secreted or transmembrane proteins TANGO 253, 1 TANGO 281 and INTERCEPT 258. These are useful in the treatment coronary, pulmonary, olfactory, immunological, neurological, developmental and kidney disorders.
                                                                                                                                                                                                                                                                                                                       Sequence 1338 BP;
                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 273;
                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acids for treating diseases and disorders, e.g. atherosclerosis, infection, autoimmune diseases, obesity, ear disorders, brain disorders, tumors, diabetes, arthritis, multiple sclerosis and asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC.
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neurological disorder; pulmonary disorder; immunological disorder;
developmental disorder; kidney disorder; ss.
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                      Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281; INTERCEPT 258; coronary disorder; olfactory disorder; neurological disorder; pulmonary disorder; immunological disorder; kidney disorder; ss.
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Disclosure;

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The present invention provides the protein and coding sequences of th human and murine secreted or transmembrane proteins TANGO 253, TANGO TANGO 281 and INTERCEPT 258. These are useful in the treatment of coronary, pulmonary, olfactory, immunological, neurological, developmental and kidney disorders.
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The invention relates to an isolated human secreted protein (SECP)
CC polypeptide from 63 fully defined protein sequences given in the
CC specification. The polypeptide is useful for the diagnosing/treating of a
CC disease with decreased/overexpression of SECP. Examples of disorders
CC disorder e.g. arterlosclerosis, cancers; autoimmune/inflammatory
CC disorder, AIDS, allergies, anaemia, asthma; cardiovascular disease e.g.
CC congestive heart failure, ischaemic heart disease; developmental disorder e.g.
CC e.g. renal tubular acidosis, hypothyroidism; neurological disorder e.g.
CC Alzheimer's disease, dementia, parkinson's disease, epilepsy or stroke.
CC the proteome of a tissue or a cell type. The polynucleotide is useful for analysing
CC creating knockin humanised animals (pigs) or transgenic animals (mice or and further for generating hybridisation probes useful in mapping the
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Lu DAM,
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09-NOV-2000;
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 CTGCCCGGGGCACCCCGGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCC
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Wala M, Thornton M, E
Hafalia AJA, Tang Y
Thangavelu K, Lee S
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Elliott VS, Lu Y, Gietze
YT, Bandman O, Warren BA
S, Xu Y, Yang J, Lal PG
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                                                                                            Ouery Match
Best Local Similarity 96.5
1042; Conservative
                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID
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23-AUG-2000;
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food supplement; medical imaging; diagnostic; genetic disorder;
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DB; ABG12724.
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Scoring table:

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Copyright (c) 1993 - 2003 Compugen Ltd.
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S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (Dipublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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             cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L/AMM1475 row: i column: 07
High quality sequence stop: 777.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                       Gene Collection (MGC)
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BF046067 BF250014A
AI083823 qf18c08 x
BM707291 UI-E-CR1-
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AI083824 qf18c09 x
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603059737
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em\_gss\_pro:\* em\_gss\_rod:\* em\_gss\_other: \* em\_gss\_mus:\* em\_gss\_mam:\* em\_gss\_vrt:\* em\_gss\_fun:\* em\_gss\_pln:\* em\_gss\_hum:\* em\_gss\_inv:\* gb\_gss:\* em\_estom: \* em\_estfun:\*

14: 15: 16: 17: 17: 18: 19: 20: 21: 22: 23: 23: 24: 25:

9: 10: 11: 12:

gb\_est2:\*
gb\_htc:\*

gb\_est4:\*
gb\_est5:\*

gb\_est3:\*

gb\_est1:\* em\_estro:\*
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em\_estin:\*

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em\_estmu:\* em\_esthum:\*

တ္ <b>က⇔ယ</b> မာမ	Result
767.8 750.6 732.8 730.2 712.6 672.2	Score
55.8 53.2 51.8 8.8	Query Match Length DB
1	Length
13 13 13	DB
13 B1763193 13 BM547549 14 BM924569 13 B1458455 13 B1490880 13 B1771879	ID
BI753193 603049929 BM547549 AGENCOURT BM924569 AGENCOURT BI458455 603198837 BI490880 603031867 BI771879 603055280	Description

TOTOTOMORPH .....

/clone\_lib="NIH\_MGC\_116" /lab\_host="DH10B" /clone="IMAGE:5190222" /organism="Homo sapiens" /db\_xref="taxon:9606"

BASE COUNT

133 a

Query Match Best Local

Similarity 97.7 53; Conservative

55.8%; 97.7%;

Score 767.8; Pred. No. 7.9 Mismatches

.9e-96;

12;

Indels

8;

DB 13; Length 869;

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251 CTCCTGGGCCTGGCCGGCCGGCTCGCCCCCCTGGACGACAACAACAACAACATCCCCAGCCTCTGC
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 CTGGTGAAGAATGGCGAATCCATTGCCTCTTTCTTCCAGTTTTTCGGGGGGTGGCCCAAG
                                                  CCTGGGGTCTACTTCGCCGTCCATGCCACCGTCTACCCGGGCCAGCCTGCAGTTTGAT
                                                                                                                GCTGGTGAAACGAGCAGGGACATTACGACGCCGTTCACCGGCAAGTTCACCTGCCAGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-*Organ: pooled colon, kidney, stomach; Vector:
pCRW-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
023. Note: this is a NIH_MGC Library.*
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KEYWORDS
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12713 row: o column: 19
High quality sequence stop: 591.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
GCCATCGGGGAGCCGGGAGGGGGGACTGCGAGAGGACCCCGGCGTCCGGGCTCCCCGGTGC
               GCCATCGGGGAGCCGGGAGGGGGGACTGCGAGAGGACCCCGGCGTCCGGGCTCCCGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BM547549
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a 382 c
                                                                                                                                                                                                                                                                                           note "Organ: ovary (pool of 3); Vector: pCMV-SPORT6; Site_1: ECORV (destroyed); Site_2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036.
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/clone="IMAGE:5724522"
/clone_lib="NIH_MGC_125"
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Pred. No. 1.5e-93;
0; Mismatches 54;
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Homo sapiens cDNA clone IMAGE:5724522
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NATIONAL INSTITUTES OF Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Upublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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                    CTGGCACAGCTCCCCAGTCTTTGCTTAGTGCCCACTGCAAAGTGAGCTCATGCTCTCACT
                                                            TGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCCGGATTTCTGGTGTACTCCGA
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Plate: LLAM12808 row
High quality sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: pooled colon, kidney, stomach; Vector: pCRV-SpORT6; Site_1: NotI; Site_2: ECORV (destroyed); RNA Source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dy primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MCC Library.*
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/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:5760942"
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Pred. No. 4.1e-91;
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REFERENCE AUTHORS TITLE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1093)

Homo

· Anthony

COMMENT

JOURNAL

ACCESSION VERSION KEYWORDS SOURCE

BM924569 BM924569.1 EST.

GI:19374948

ORGANISM

Homo sapiens

uman.

RESULT 3 BM924569

DEFINITION

AGENCOURT\_6767665 NIH\_MGC\_116

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cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Segmenting by: The I.M.A.G.E. Consortium (LLNL)	
	Db 19 TCCTCTTGGAGTCTGGGAGGAGGAAGCGGAGCGGAGCGAACCAGGACTGGGGT 78
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homc 1 (bases 1 to 801) NIH-MGC http://mgc.nci.nih.gov/.	Query Match Best Local S Matches 803
BI49080.1 GI:15330108 EST. human. H.M. Homo sapiens	constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."  ORIGIN  129 a 271 c 330 g 115 t 1 others
RESULT 5 BI490880/c BI490880 LOCUS BI490880 BI490880 BI490880 BEFINITION 603031867T1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5172880 3', BI49080 BI49080 BI490800 BI490800 BI490800 BI490800 BI490800 BI4908000 BI490800000000000000000000000000000000000	KS+); Site_1: Bam! KS+); Site_1: Bam! primed using prime ed for average ins to ROT 5. This is a to ROT 5. This is a
Oy 786 AGCCAGCCTCGCTCGGGGGGGGGCCATGGTGAGGCTGGAGGACCAAGTG 841 Db 793CAGGCAAGCTCGTCTCGGGGGGGGCATGTTGAGGCTGGAGCTTGAGACCAGTGTG 846	/clone="IMAGE:5278184" /clone_tb="NIH_MGC_96" /tissue_type="hypothalamus" /lab_bost="DH108"
Db 737 ATCTGGTGAAGAATGGCGAATCCATTGCCTCTTTCTTCCAGTTTTTCGGGGGGGTGGCCCA 785	Source 1. 846  /db_xref="taxon:9606"
678	* n = -
618	yuki and Piero Carninci (RIKEN) Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) equencing by: Incyte Genomics, Inc. distribution: MCC clone distribution information can
547	rt Strausberg, Ph.D. -r@mail.nih.gov ament: Miklos Palkovits, M.D.; Ph.D. Preparation: Michael J. Brownstein (NHGRT)
487 499	CE 1. (bases 1 to 846)  RS NIH-MGC http://mgc.nci.nih.gov/.  National Institutes of Health, Mammalian (Appublished (1999)
QY 427 GGGCGGGAGGCCGGGACCTCGAGGGGACCCCGGGCCGCGGGGAGAGGCGGG 486	human.  Homo sapiens  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E  Mammalia; Eutheria; Primates; Catarrhini. Hominidae.
Qy 367 GGGCCGCGATGGCCGCGACGGCGCGCGCGCGCGCGCGCGC	MRNA sequence.  ION BI458455  N BI458455.1 GI:15249111  DS EST.
307 319	RESULT 4  BI458455  BI458455  BI458455  LOCUS  BI458455  BI45845  BI45845
Qy 247 GCTGCTCCTGGGCCTGGGGCCGGCCCCCACTGGACGACAACAAGATCCCCAGCCT 306	Db 781 GG 782.
QY 187 GCGAGAGGACCCCGGCGTCCGGGCTCCCGGGTGCCAGCGCTATGAGGCCACTCCTCGTCCT 246	Db 721 ATATTGTGAATGACTAGGGAAGGGGGGTANAANCACTCTCCGTCCCTGCTGCCAA 780  1110 TG 1111
Db 139 GGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGGACT 198	Db 661 CCTAGAAAGGAGGTGTGAGGCTGACACCCAGGTCATCCAGGAGGCCTGGGCCCCCTGGA.720  97 1050 ATATTGTGAATGACTAGGGAGGTGGGGTGAGACCAGTCTCCTCCTGCTCCTCCTACCAA.720

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Query Match
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                                                   GTGTGAGGCTGACAACCAGGTCATCCAGGAGGGCTGGCCCCCCTGGAATATTGTGAATGA 1062
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Similarity 98.2%;
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pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
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                                                                                                                                                                          Similarity
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies,
                                                 High quality sequence stop: 672
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Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 724)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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mRNA sequence.
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                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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/clone="IMAGE:5204971"
/clone_lib="NIH_MGC_122"
                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    'lab_host-"DH10B"
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Pred. No. 9.2e-83;
0; Mismatches 4
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                                                              http://image.llnl.gov
Plate: LLAM12785 row: n column:
High quality sequence stop: 415.
Location/Qualifiers
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                                                                                                        cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies,
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1 (bases 1 to 1045)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BM920874.1 (
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                /Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5752141"
/clone_11b="NIH_MGC_115"
/lab_host="DH10B"
       pooled brain,
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Pred. No. 1.1e-82;
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BI770921 603059737F1 NIH\_MGC\_122

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Query Match
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Plate: LLAM11524 row: j column: 10
High quality sequence stop: 782.
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                    GTACTCCGACTGGCACAGCTCCCCAGTCTTTGCTTAGTGCCCACTGCAAAGTGAGCTCAT
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                       GCAGGGACATTACGACGCCGTCACCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTA 681
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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                      CTTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGG
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1 (bases 1 to 792)
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                             High quality sequence stop:
                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 887)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                    /organism="Homo sapiens"
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/clone="IMAGE:5172880"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/note-*Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb Library is normalized and enriched for full-length clones and was constructed by C
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ns cDNA clone IMAGE:5172880
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EST 28-AUG-2001

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720

1216 660

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Market Control

BASE COUNT ORIGIN

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REFERENCE AUTHORS TITLE

COMMENT

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ACCESSION VERSION KEYWORDS

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EST 12-MAR-2002 IMAGE: 5766864

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                               CCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTACATTGGCATCTATGCCAGCATCAAGAC
                                                                                  GGGGTGGCCCAAGCCAG-CTCGCTCTCGGGGGGGGGCCATGGTGAAGCCTGGAGCCTGAAGGA
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277 c 307 g 157 t
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Pred. No. 1.1e-78;
0; Mismatches 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1623)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
CCGGGGCACCCCGGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGC
                                                                                                                                                                                                                                                                     Similarity
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Plate: LLAM12824 row: d column:
High quality sequence stop: 558.
                                                                                                                                    GGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGACTGCGA
                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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BM926477
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ilarity 100.0%; Pred. No. 2.4
Conservative 0; Mismatches
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63 a 505 c 550 g 299 t 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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/clone="IMAGE:5766864"
/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
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                                                                                                                                                                               Email: cgapbs remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), S
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10678 row: 1 column: 23
High quality sequence stop: 630.
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NH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_96"
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/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhOI (gtcgag pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhOI (gtcgag ); Oligo-dT primed using primer 5. "TriTTTTTTTTTTTTTTTTTTVN-3; size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
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Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
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1)26g10.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo CDNA clone IMAGE:6136122 3' Similar to TR:Q9UFX4 Q9UFX4 HYPOTHETICAL 22.8 KD PROTEIN ;, mRNA sequence.
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Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
             GGAACAGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTTGGCTGGATTTCTGCCC
                                                                                                                                                                                                    TGGCACAGCTCCCCAGTCTTTGCTTAGTGCCCACTGCAAAGTGAGCTCATGCTCTCACTC 991
                                                                           ATTGTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGTCCTGCTGCTGGCAAGGAATG
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity,
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Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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/db_xref="taxon:9606"
/clone="IMAGE:6136122"
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cDNA Library Arrayed by: The I.M.A.G.E. Consorttum (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://image.llnl.gov
Plate: LLAM12357 row:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                       /note-*Organ: Ovary (pool of 3); Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."
                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:5587759"
/clone_lib="NIH_MGC_125"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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                                                                                                                                                                   Score 586.4; DB Pred. No. 5e-71;
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11440 row: p column: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                      BM893691 578 bp mRNA linear EST 29-APR-2002 1j28e08.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo saplens cDNA clone IMAGE:6136046 3' similar to TR:Q9UFX4 Q9UFX4 HYPOTHETICAL 22.8 KD PROTEIN ;, mRNA sequence.
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Query Match Best Local S Matches 578  Qy 770  Db 578  Qy 830  Db 518  Qy 890  Db 458	BASE COUNT	FEATURES Source	TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS
Ch 42.0%; Score 578; DB 14; Length 578; 1 SImilarity 100.0%; Pred. No. 7.1e-70; 578; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 70 TTCGGGGGGTGGCCCAAGCCAGCCTCGCTCTCGCGGGGGCCATGGTGAGGCTGGAGCCT 829 [	130	Pept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138  Tel: 617-495-1812  Fax: 617-495-8557  Email: dmeltonebiohp.harvard.edu Library was constructed by Dr. Douglas Melton DNA sequencing by: Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center For information on Obcom@ffs.harvard.edu) Seq primer: -40Up from Gibco High quality sequence stop: 408. Location/Qualifiers 1. 578 //Clone="IMAGE:6136046" //Clone="IMAGE:6136046" //Clone="IMAGE:6136046"	Hiller, L., Marra, M., Pape, D., Wyller, T., Martin, J., Blistein, R., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.  Endocrine Pancreas Consortium Unpublished (2000) Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium	BM893691.1 GI:19349159 EST. human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 578) Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,

950 TTTGCTTAGTGCCCACTGCAAAGTGAGCTCATGCTCTCACAGAGAGGAGGGTGTGAG 1009
3 5 9 5 1 1 2 1 2 1 3 1

Search completed: June 22, 2003, 05:15:25 Job time : 1908 secs

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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
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US-09-336-536-8
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US-09-188-930-218
US-09-188-930-30
US-09-188-930-30
US-09-136-536-74
US-09-136-536-74
US-09-136-536-74
US-09-140-804-29
US-09-140-804-29
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US-09-140-804-31
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US-09-140-804-31
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US-09-140-804-31
US-09-13-840A-1
US-09-056-556-182
US-09-072-596-177
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4 US-09-073-683-744-1
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APPLICANT: Humes, Jacqueline M.

TITLE OF INVENTION. ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS

FILE REFERENCE: 97-49

CURRENT APPLICATION NUMBER: US/09/140,804

CURRENT FILING DATE: 1998-08-26

EARLIER APPLICATION NUMBER: 60/056,983

EARLIER FILING DATE: 1997-08-26

NUMBER OF SED ID NOS: 47

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO. 1
                                                                                                                                                                                                                                                                                           LENGTH: 1347

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (198)...(926)
US-09-140-804-1
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Best Local Similarity
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US-09-230-371A-16
US-09-18-408-1
US-09-18-408-1
US-09-103-840A-1
4 US-09-103-840A-2
US-09-103-840A-2
US-09-397-787-161
US-08-690-473-1
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US-08-843-659-1
US-08-843-659-1
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Pred. No. 5.7e-257;
0; Mismatches 3;
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6-536-1	1271 GGGGCCGGCCCTTTTCTCAGAGATCACTCAATAAACCTAAGAACCCTCAAAAAAAA	1240 TGGGGTGCTCTTTCCTCGGTCCTCTGCTTCTCTGGATCCTCCCACCCCCTCCTGCTCCT 1299 1111111111111111111111111111111111	THE INTEGRATICAGGTCTGGCAGCARGGGGGGGGGGGGGGGGGGGGGGGGG	971 AGGGTGGAGGCTGACAACCAGGTCATCCAGGAGGGCTGGCCCCCCTGGAATATTGTGAA 1039 1060 TGACTAGGAAGGTGAGGACACTCTCCGTCCTGCTGCTGCCAAGGAATGGGAACAGT 1119 111111111111111111111111111111111	999	GCTGGAGCATCAAGACAGCACGCTCTCCCGGATTTTTTTT		640 CGTCACCGCCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTTCGCCGTCCATGCCAC 699 611 CGTCACCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTACTTCGCCGTCCATGCCAC 699 611 CGTCACCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTACTTCGCCGTCCATGCCAC 670 700 CGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGAATCCATTTGTCTTTT 750	GTCTGACGCACCCTTGCCCTTCGACCGCGTGCTGGTGAACGAGCAGGGACATTACGACGC	431 GGACCCCGGGGATG 519 431 GGACCCCCGGGGACTG 519 431 GGACCCCCGGGCACGGGACTG 519 520 CTCGGTGCCTCCGCGTTCAGCGCCAAGCGCTCCGAGACTG 490 520 CTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTCCGAGAGCGGTGCCTCCGCC 579 111111111111111111111111111111111111	
GGGGGTG         GGGGGTG	OY 654 TCACCTRCCAGGTGCCTGGGGTCTACTACTTCGCCGTCCATGCCACCGTCTACCGGGCCA 713	494 GATCCGC 594 TGCCCTT		Oy         354         GCCAGGGCTTGCCGGGCCCGGACGGCCGCGACGGCGCGCGGGGCTCCGG         413           Db         315         GCCAGGGCTTGCCGGGCCGCGATGGCCGCGACGGCGCGCGC	Db 195 CACTCCTGCTGCTGCTGCTGCGCCGGGGCTGGCCCACTGACACAACA 254  Qy 294 AGATCCCCAGCCTCTGCGGGGACGACGGCCTCGGCCCACTGGACGACACA 353		OY 54 CCAGGACTGGGGTGACGCCAGGGGGGGCCTGGCCGGGAGAAGCGCGGGGGCTGG 113	Query Match Best Local Similar Matches 1310; Cor	; SEQ 1D NO 1 ; LENGTH: 1338 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-336-536-1	TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF FILE REFERENCE: 7853-144 CURRENT APPLICATION NUMBER: US/09/336,536 CURRENT FILING DATE: 1999-06-18 NUMBER OF SEQ ID NOS: 75 SOFTWARE: Patentin Ver. 2.0	; Sequence 1, Application US/09336536; Patent No. 6406884; GENERAL INFORMATION: APPLICANT: Leaby, K. APPLICANT: McKay, C. APPLICANT: McKay, C. C. APPLICANT: McKay, C.

RESULT 2 US-09-336-536-1

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Sequence 2, Application US/09336536

Patent No. 6406884

GENERAL INFORMATION:
APPLICANT: Letby, K.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USI
FILE REFERENCE: 7853-144
CURRENT FILING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 75
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 728
TYPE: DNA
ORGANISM: Homo sapiens
US-09-336-536-2
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US-09-336-22
Sequence 2, App
Patent No. 6400
GENERAL INFORM
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                                    GACAACAAGATCCCCAGCCTCTGCCCGGGGCACCCCGGGCCTTCCAGGCACGCCGGGCCAC
                                                                  GGGTAGAGCACTCTCCGTCCTGCTGCTGGCAAGGAATGGGAACAGTGGCTGTCTGCGATC
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Pred. No. 1.4e-135;
0; Mismatches 0;
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PATCHT NO. 6406884
GENERAL INFORMATION:
APPLICANT: Lelby, K.
APPLICANT: HORAY, C.
APPLICANT: MCRAY, C.
APPLICANT: BOSSONG, S.
TITLE OF INVENTION: SECRETED PROTEINS AN
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                                                                                               ; LENGTH: 1263
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-336-536-8
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                                                                                                                    CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 1263
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                                                              50.3%;
nilarity 78.0%;
Conservative
                                                             Score 692.8; DB 4;
Pred. No. 1.1e-130;
0; Mismatches 237;
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GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Strachan, Lorna

APPLICANT: Strachan, Matthew

APPLICANT: Onrust, Rene

APPLICANT: Onrust, Rene

APPLICANT: Murison, James Greg

TITLE OF INVENTION: Compositions Isolated From Skin Cells

TITLE OF INVENTION: and Methods For Their Use

FILE REFERENCE: 11000.1011c1

CURRENT APPLICATION NUMBER: US/09/188,930A

CURRENT FILING DATE: 1998-11-09

SOFTWARE: FASTSEQ FOR Windows Version 3.0

LENGTH: 1001

TYPE: DNA
ORGANISM: Rat
US-09-188-930-218
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US-09-188-930-218
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: Patent No. 6150502
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Best Local Similarity
Matches 739; Conserv
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          CCTTCAGCGCCAAGCGCTCCGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCTTGCCCT
                                                                                AGGCGGGACCCGCGGGGCCACCGGGCCTGCCGGGGGAGTGCTCGGTGCCTCCGGGATCCG
                                                                                                       GTCTGAGGAAGCCATTCAAAGCGAGCAGCTGGGAAGGGTGGGAAGGGGCCTAC
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                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                          44.0%; Score 606; DB 3; Length 10
78.6%; Pred. No. 2.7e-113;
vative 0; Mismatches 195; Indels
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RESULT 6 US-09-188-930-30

Sequence 30, Appli Patent No. 6150502

INFORMATION:

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931 960 871 900 811 840 751

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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
UNUMBER OF SEQ ID NOS: 348
SOFTMARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: (545)...(545)
-09-188-930-30
                                                                                                                                    165 AGACTACAAGAGAGGATCCTGGGCTTCGGCCCTCGGGTCATCACCATGAGGCCACTTC
                                                                                                                                                186 TG-----CGAGAGGACCCCGGCCTCCCGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCC
                                                                                                                                                                                                                                 66 TGACGGCAGGGCAGGGGGGCCCTGGCCGGGGAGAACGCGCGGGGGCTGGAGCACCACCACC
                                                                                                                                                                                                                                                                   similarity 78.5%;
Similarity 78.5%;
38; Conservative
           CCAGCCTCTGCCCGGGGCACCCCGGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGG
                                                                                           GTCTGAGGAAGCCATTCAAAGCGAGCAGCTGGGAGAGCTGGGGAGGCCGGGAAGGGCCTAC
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                                                                                                                                                                                                                                                                  Score 605; DB 3;
Pred. No. 4.3e-113;
0; Mismatches 196;
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                                                                                                                                                   APPLICANT: Lebby K.
APPLICANT: McKay, C.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND US
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT EILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 729
LENGTH: 729
LENGTH: 729
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TYPE: DNA

ORGÂNISM: Mus π
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US-09-336-536-9
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                                                                                                   Query Match
Best Local
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                                                                                           Matches
                                                                                                                                                                                                                                                                                           Sequence 9, Application US/09336536 Patent No. 6406884
                                         287
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                                                                                     Similarity 85.9
26; Conservative
GACAACAAGATCCCCAGCCTCTGCCCGGGGCACCCCGGCCTTCCAGGCACGCCGGGCCAC 346
                                                                                                                                                                                                                                                                                                                                                                                                                                     ATACAGTGAACCCGGAGCTGGCACTTGCTCCTAGTGGAGG
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                                                                                                                                            musculus
                                                                                               41.0%;
                                                                                      0;
                                                                                    Score 564.2; DB 4;
Pred. No. 6.2e-105;
0; Mismatches 103;
                                                                                     Indels
                                                                                                        Length 729;
                                                                                   0
                                                                                  Gaps
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Query Match Best Local Sim Matches 738;

45

LENGTH: 1015 TYPE: DNA ORGANISM: Rat FEATURE:

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APPLICANT: Humes, Jacqueline M.

APPLICANT: Humes, Jacqueline M.

TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS

FILE REFERENCE: 97-49

CURRENT APPLICATION NUMBER: US/09/140,804

CURRENT FILING DATE: 1998-08-26

EARLIER APPLICATION UMBER: 60/056,983

EARLIER FILING DATE: 1997-08-26

NUMBER OF SEQ ID NOS: 47

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 10

LENGTH: 729

TYPE: DNA

COCCURRENT APPLICATION SECURED SECURE
                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
US-09-140-804-10
            Query Match
Best Local S
Matches 419
                                                                                                                                                                                                                                                                                                                              Sequence 10, Applicate Patent No. 6197930 GENERAL INFORMATION:
                                                                           FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                     ORGANISM: Artificial Sequence
         al Similarity 57.6%;
al Similarity 57.6%;
419; Conservative 14
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         145;
      Score 504; DB 4;
Pred. No. 7.5e-93;
45; Mismatches 164
                                                                             sequence
NO:2.
      164;
                              Length 729;
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    Indels
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 Gaps
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                                                 APPLICANT: Leiby, K.
APPLICANT: McRay, C.
APPLICANT: McRay, C.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND US
FILTE REFERENCE: 7853-144
CURRENT APPLICATION UNMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 74
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       LENGTH: 60
TYPE: DNA
ORGANISM:
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1 GTNTTYGC 728
      Rattus norvegicus
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946 660 886 600 826 540 766 480

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Sequence 26, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Steachan, Lorna
APPLICANT: Steachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Ski
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000,1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH- 205
                                                                                          ; TYPE: DNA
; ORGANISM: Rat
US-09-188-930-26
                                                                                                                                                                                                                                                                                                                                                                                                           US-09-188-930-26
                         Query Match
Best Local Similarity 69.1
Matches 250; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 18.7%;
Best Local Similarity 72.0%;
Matches 365; Conservative
                                                                                                                                        LENGTH:
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                                         10.9%;
                       Score 149.6; DB 3
Pred. No. 8.6e-22;
0; Mismatches 104
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Pred. No. 1.8e-43;
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US-08-463-911-1
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                                                                                                  TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1276 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TELECOMUNICATION IMPORMATION:
TELEPHONE: (617) 861-6240
                                         MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/463,91
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook,
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Scherer, Philipp E.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
                                                                                 STRANDEDNESS:
                            NAME/KEY:
                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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US-08-463-911-6
                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08463911 Patent No. 5869330 GENERAL INFORMATION:
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Best Local Similarity
       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                          APPLICANT: Scherer, Philipp E.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C
                                                                                                                              STATE: Massachusetts
COUNTRY: USA
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                                                                                                                                                                                 Two Militia Drive
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51.5%;
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Pred. No. 7.3e-10;
0; Mismatches 279;
                            Version #1.30
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; LOCATION:
US-08-463-911-6
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Best Local Similarity 50.1%;
Matches 316; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
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TYPE: nucleic acid
STRANDEDNESS: single
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Pred. No. 3.6e-08;
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SOFWARE: FRATSEQ for Windows Version 3.0
: SEQ ID NO 9
: LENGTH: 4517
TYPE: DNA
: ORGANIZM: Homo sapiens
US-09-140-804-9
Sequence 23, Application US/09118408A Patent No. 6265544 GENERAL INFORMATION:
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Best Local Sin
Matches 316;
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CURRENT APPLICATION NUMBER: US/09/140,804

CURRENT FILING DAYE: 1998-08-26

EARLIER APPLICATION NUMBER: 60/056,983

EARLIER FILING DAYE: 1997-08-26

NUMBER OF SEQ ID NOS: 47
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APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
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Similarity 50.1%;
16; Conservative
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Pred. No. 4.4e-08;
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TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN
FILE REFERENCE: 97-30
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OTHER INFORMATION: Each N is independently any nucleotide
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ORGANISM: Artificial Sequence
FEATURE:
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888 TCAAGACAGACACCTTCTCCGGATTTCTCGTGTA 924
                               731 AYCARGINIGGINMGNYINTAYAARGGNGARMGNGARAAYGCNAIHTIYWSNGARGARY
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                                                                                            ARGTNGGNGAYMGNWSNATHATGCARWSNCARWSNYTNATGYTNGARYTNMGNGARCARG
                                                                                                                         ARAARGARACNTAYYTNCAYATHATGAARAAYGARGARGARGTNGTNATHYTNTTYGCNC
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                                                           CTGAGGACCAAGTGTGGGTGCAGGTGGGTGGGTGACTACATTGGCATCTATGCCAGCA
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30.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 77.4; DB 4; Length 8; Pred. No. 3e-07; 99; Mismatches 384; Indels
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: LOCATION: (1)...(843)

: OTHER INFORMATION: Each N is independently any nucleotide

US-09-506-855-23
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Best Local Similarity 30.0
Matches 209; Conservative
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CURRENT FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 50
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23
LENGTH: 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23, Application US/09506855
Patent No. 6448221
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Lasser, Gerald W.
APPLICANT: Bishop, Paul D.
TITTE CO TANGENTY. Paul D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND FILLE OF INVENTION: IMMUNE FUNCTION FILLE REFERENCE: 99-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Degenerate nucleotide sequence encoding zsig37 OTHER INFORMATION: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                              491 CNGTNATHTTYGAYACNGARTTYGTNAAYYTNTAYGAYCAYTTYAAYATGTTYACNGGNA 550
                                                                                                                                                                                                                                                                                                                                                             431 AYTAYGCNGCNTTYWSNGTNGGNHGNAARAARCCNATGCAYWSNAAYCAYTAYTAYCARA 490
                                                                                                                                                                                                                                                                                                                                                                                                        531 CGCGATCCGCCTTCAGCGCCAAGCGCTCCGAGAGCCGGGTGCCTCCGCCGTCTGACGCAC 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                         371 AYACNGGNCCNAARGGNCARAARGGNWSNATGGGNGCNCCNGGNGARMGNTGYAARWSNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411 CGGGAGAGAAAGGCGAGGGGGGAGCCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGC 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353 AGCCAGGGCTTGCCGGGCCGCGA--TGGCCGCGACGGCCGACGGCGCGCGCGCGCGCTC 410
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ARGTNGGNGAYMGNWSNATHATGCARWSNCARWSNYTNATGYTNGARYTNNGNGARCARG 730
                                         ARAARGARACNTAYYTNCAYATHATGAARAAYGARGARGARGTNGTNATHYTNTTYGCNC
                                                                                                                    CCTTGCCCTTCGACCGCGTGCTGGTGAACGAGCAGGACATTACGACGCCGTCACCGGCA 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCGAGGAGAGGGGGACCCGCGGGGGCCCACCGGGGCCTGCCGGGGAGTGCTCGGTGCCTC 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGATCCCCAGCCTCTGCCCGGGGCACCCCGGGCCTTCCAGGCACGCCGGGCCACCATGGC 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARGAYCARGGNYTNCCNGCNWSNWGNTGYYTNWGNTGYTGYGAYCCNGGNACNWSNATGT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.6%; Score 77.4; DB 4; Length 843; 30.0%; Pred. No. 3e-07; tive 99; Mismatches 384; Indels
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731 AYCARGINIGGGINMGNYINTAYAARGGNGARMGNGARAAYGCNATHITYWSNGARGARY 790
                                                                828 CTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTACATTGGCATCTATGCCAGCA 887
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Search completed: June 22, 2003, 05:17:19 Job time: 106 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
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                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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1377
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                                                                                                                                                              //ggn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
//ggn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
//ggn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
//ggn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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SUMMARIES
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Result	Score	Query Match	Query Match Length DB	æ	ID	Description
<u></u>	1377	100.0	1377	: و	US-09-944-413-41	Sequence 41. Appl
N	1377	100.0	1377	9	US-09-944-403-41	41.
w	1377	100.0	1377	9	US-09-944-896-41	41
4	1377	100.0	1377	9	US-09-944-944-41	4
σ	1377	100.0	1377	φ	US-09-944-907-41	41
σ	1377	100.0	1377	9	US-09-944-929-41	
7	1377	100.0	1377	ဖ	US-10-028-072-361	361
8	1377	100.0	1377	9	US-10-121-049-361	361
9	1377	100.0	1377	9	US-10-123-904-361	361
10	1377	100.0	1377	9	US-10-140-470-361	361
Ξ	1377	100.0	1377	9	US-10-175-746-361	361
12	1377	100.0	1377	9	US-10-176-918-361	361
13	1377	100.0	1377	9	US-10-176-921-361	361
14	1377	100.0	1377	9	US-10-137-865-361	361
15	1377	100.0	1377	9	US-10-140-474-361	361
16	1377	100.0	1377	9	US-10-142-431-361	361
17	1377	100.0	1377	ø	US-10-143-114-361	361
18	1377	100.0	1377	9	US-10-140-002-361	361
19	1377	100.0	1377	9	US-10-142-419-361	161

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US-10-123-910-361	US-10-123-909-361	-10-12	US-10-123-902-361	-10-12	-10-12	-10-12	US-10-121-041-361	ò	÷	US-10-140-925-361	1	US-10-124-819-361	1	Ξ	Ļ	Ļ	US-10-140-921-361	Ļ	Ļ	÷	US-10-143-032-361	US-10-141-755-361	US-10-121-050-361	-10-14	TOC-707-571
	Sequence	Sequence	Sequence	•••														-		-	•••	Sequence	Sequence	Sequence	sequence
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## ALIGNMENTS

RESULT 1 US-09-944-413-41

	; PRIOR APPLICATION NUMBER: 60/069,278; PRIOR FILING DATE: December 11, 1997; PRIOR APPLICATION NUMBER: 60/069,425; PRIOR APPLICATION NUMBER: 60/069,696; PRIOR APPLICATION NUMBER: 60/069,696; PRIOR APPLICATION NUMBER: 60/069,694; PRIOR APPLICATION NUMBER: 60/069,694; PRIOR APPLICATION NUMBER: 60/069,694; PRIOR FILING DATE: December 16, 1997; PRIOR FILING DATE: December 16, 1997	OF INVENTION: ACIDS ENERFERENCE: P2548P1C1 NT APPLICATION NUMBER: 0201-03 APPLICATION NUMBER: 09, FILING DATE: 2001-05-22 APPLICATION NUMBER: 60, FILING DATE: December : APPLICATION NUMBER: 60, FILING DATE: December : APPLICATION NUMBER: 60, FILING DATE: December : APPLICATION NUMBER: 60,	APPLICANT: Goddard, Audrey APPLICANT: Godowski, Paul APPLICANT: Gofowski, Paul APPLICANT: Gurney, Austin APPLICANT: Gurney, Austin APPLICANT: Hillan, Kenneth APPLICANT: Kljavin, Ivar APPLICANT: Kljavin, Ivar APPLICANT: Napler, Mary APPLICANT: Roy, Margaret APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Mood, William TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE	Ty US FOR
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Query Match 100.0%; Score 1377; DB 9; Length 1377; Best Local Similarity 100.0%; Pred. No. 0; Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Oy 1 GACTAGTTCTCTTGGAGTCTGGGAGGAGGGAAGCGAGGGAGCGAAGCAGGAC 60	: LENGTH: 1377 : TYPE: DNA : ORGANISM: Homo Saplen US-09-944-413-41	CATION N	****	; PRIOR ELLIATION NUMBER: PCT/US00/08439 ; PRIOR ELLIAG DATE: March 30, 2000 ; PRIOR APPLICATION NUMBER: PCT/US00/14042 ; PRIOR FILING DATE: May 22, 2000	FILING DATE: February 22 APPLICATION NUMBER: PCT, APPLICATION NUMBER: PCT, FILING DATE: March 2, 20	APPLICATION NUMBER: PCT, FILING DATE: December 10 APPLICATION NUMBER: PCT, FILING DATE: February 11	APPLICATION NUMBER: PCT FILING DATE: NO. US20020 APPLICATION NUMBER: PCT FILING DATE: December1,	APPLICATION FILING DATE FILING DATE	FILING DATE: March 3 APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: June 22	APPLICATION FILING DATE APPLICATION FILING DATE	FILING DATE: Septem APPLICATION NUMBER APPLICATION NUMBER FILING DATE: December 1	APPLICATION NUMBER FILING DATE: December APPLICATION NUMBER FILING DATE: July	R FILING DATE: February R APPLICATION NUMBER: 60, R APPLICATION NUMBER: 60, R FILING DATE: December 1	FILING DATE: February ( APPLICATION NUMBER: 60) FILING DATE: February ( FILING DATE: February (	FILING DATE: December APPLICATION NUMBER: 60 FILING DATE: January 5	FILING DATE: December APPLICATION NUMBER: FILING DATE: December FILING DATE: December Decembe	APPLICATION NUMBER: 60/069,70 FILING DATE: December 16, 199
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1021 GGTCATCCAGGAGGCTGCCCCCTGGAATATTCTGAATCACTAGGAGGTCGGGTAGA 1080	<b>⊢</b> ⊢	901 CACCTTCTCCGGATTTCTGGTGTACTCCGACTGGCACAGCTCCCCAGTCTTTGCTTAGTG 960 	841 GTGGGTGCAGGTGGGTGAGTACATTGGCATCTATGCCAGCATCAAGACAGAC	781 GCCCAAGCCAGCCTCGCTCTCGGGGGGGGCCATGGTGAAGGCTGGAGGCCTGAGGACCAAGT 840	721 GTTTGATCTGGTGAAGAATGGCGAATCCATTGCCTCTTTCTT	661 CCAGGTGCCTGGGGTCTACTTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCA 720	601 CGACCGCGTGCTGGTGAACGAGCAGGGACATTACGACGCCGTCACCGGCAAGTTCACCTG 660 	541 CTTCAGCGCCAAGCGCTCCGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCTTGCCCTT 600 	481 GGCGGGACCCGCGGGCCCACCGGGCCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGC 540	421 AGGCGAGGGCGGGAGGCGGGACTGCCGGGACCTCGAGGGGACCCCGGGGCGCGAGGAGA 480	361 CTTGCCGGGCCGCGATGGCCGCGACGGCGCGCGCGCGCGGGGCTCCGGGAGAGAA 420	301 CAGCCTCTGCCCGGGCACCCCGGCCTTCCAGGCACGCGGGCCACCATGGCAGCGAGGG 360 	241 CGTCCTGCTGCTCCTGGGGCCTGGGGCCGCCCCACTGGACGACAACAAGATCCC 300 	181 GGGACTGCGAGAGGACCCCGGCGTCCGGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCT 240	121 CCAACTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGG 180	61 TGGGTGACGCAGGGCAGGGGCCCTGGCCGGGGAGAAGCGCGGGGGGCTGGAGCACCA 120	1 GACTAGTTCTCTTGGAGTCTGGGAGGAGGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGAC 60

RESULT 2 US-09-944-403-41

Sequence

sequence 41, Application US/09944403

INFORMATION

Botstel

ln,David Napoleone

Kevin

APPLICANT

Goddard, Audrey Filvaroff, Ellen

Grimaldi, Christopher Godowski, Paul Gerritsen, Mary

PPLICANT:

Kljavin, Ivar Gurney, Austin

Tumas, Daniel Wood, William

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,403
CURRENT FILING DATE: 2001-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1141 GCAGCATGGGCAGTGGCTGGATTTCTGCCCAAGACCAGAGGAGTGTGCTGTGCTGGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1141 GCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCAGAGGAGTGTGCTGTGCTGGCAA 1200
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; ORGANISM: HOMO
US-09-944-403-41
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 1377; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID
SEQ ID NO 41
LENGTH: 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IOR APPLICATION NUMBER: 09/254,311
IOR FILING DATE: March 3, 1999
IOR APPLICATION NUMBER: PCT/US99/12252
IOR APPLICATION NUMBER: PCT/US99/21090
IOR APPLICATION NUMBER: PCT/US99/21090
IOR FILING DATE: September 15, 1999
IOR APPLICATION NUMBER: PCT/US99/28409
IOR FILING DATE: NO. US20020165143Alember 30, 1999
IOR APPLICATION NUMBER: PCT/US99/28313
IOR FILING DATE: NO. US20020165143Hember 30, 1999
IOR APPLICATION NUMBER: PCT/US99/28301
IOR FILING DATE: NO. US20020165143Alember 30, 1999
IOR APPLICATION NUMBER: PCT/US99/28301
IOR FILING DATE: December1, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: December 1, 2000 APPLICATION NUMBER: PCT/US01/06520
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FILING DATE: May 22, 2000
APPLICATION NUMBER: PCT/US00/20710
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FILING DATE: February 22, 2000
APPLICATION NUMBER: PCT/US00/05841
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FILING DATE: December 16, 1998
APPLICATION NUMBER: 09/218,517
FILING DATE: December 22, 1998
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FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
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PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR PRIOR PAPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,69,69,400
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,870
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OR FILING DATE: December 17, 19
OR APPLICATION NUMBER: 60/069, 8
OR FILING DATE: December 17, 19
OR APPLICATION NUMBER: 60/068, 0
OR FILING DATE: December 18, 19
OR APPLICATION NUMBER: 60/070, 4
OR FILING DATE: January 5, 1998
OR APPLICATION NUMBER: 60/074, 0
OR APPLICATION NUMBER: 60/074, 0

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NUMBER: 60/070,440

February

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CURRENT APPLICATION UNMBER: 09/08/34

PRIOR APPLICATION UNMBER: 09/08/33

PRIOR FILING DATE: DOCUMENT: 11, 1997

PRIOR APPLICATION INMBER: 60/08/278

PRIOR FILING DATE: DOCUMENT: 1, 1997

PRIOR FILING DATE: DOCUMENT: 1, 1997

PRIOR APPLICATION NUMBER: 60/08/278

PRIOR FILING DATE: DOCUMENT: 1, 1997

PRIOR APPLICATION NUMBER: 60/08/278

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APPLICANT: Baker,
APPLICANT: Botste
APPLICANT: Eaton;
APPLICANT: Ferrar
APPLICANT: Filvar;
APPLICANT: Goddar;
APPLICANT: Godows)
APPLICANT: Gorimal,
APPLICANT: Gurney
APPLICANT: Hillan,
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Patent No. US20020168715A1
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Tumas, Daniel
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Goddard, Audrey
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APPLICATION FILING DATE

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Query Match 100.0%; Score 1377; Best Local Similarity 100.0%; Pred. No. 0; Matches 1377; Conservative 0; Mismatches
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(OR APPLICATION NUMBER: PCT/US00/04414
(OR FILING DATE: February 22, 2000
(OR APPLICATION NUMBER: PCT/US00/05841
(OR FILING DATE: March 2, 2000
(OR APPLICATION NUMBER: PCT/US00/08439
(OR APPLICATION NUMBER: PCT/US00/14042
(OR APPLICATION NUMBER: PCT/US00/14042
(OR APPLICATION NUMBER: PCT/US00/20710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OR FILING DATE: September 15, 1999
OR APPLICATION NUMBER: PCT/US99/28409
OR FILING DATE: NO. US20020168715Alember 30
OR APPLICATION NUMBER: PCT/US99/28313
OR FILING DATE: NO. US20020168715Alember 30
OR APPLICATION NUMBER: PCT/US99/28301
OR APPLICATION NUMBER: PCT/US99/28301
OR ETLING DATE: December 1, 1999
OR APPLICATION NUMBER: PCT/US99/30095
OR FILING DATE: December 16, 1999
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: September 15, 1999
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FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
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      AGGCGAGGCGGGAGGCCGGGACTGCCGGGGACCTCGAGGGGACCCCCGGGGCCGCGAGGAGA
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NOS: 120
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Sequence 41, Application US/09944944
Patent No. US20020173463A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
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NUMBER OF SEQ ID SEQ ID NO 41 LENGTH: 1377

TYPE: DNA
ORGANISM: Homo Sapien
09-944-896-41

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241

Gurney, Austin Hillan, Kenneth Grimaldi, Christopher Gerritsen, Mary Goddard, Audrey

Kljavin, Ivar

Napier, Mary

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PIC1
CURRENT APPLICATION UMBER: US/09/944,944
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/86,028
PRIOR FILLING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILLING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILLING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,35
PRIOR FILLING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
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PRIOR APPLICATION NUMBER: 60/069,278
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PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR APPLICATION NUMBER: 60/069,696
                                                                                                                                                                                                                                                                                                                                                                                                                                        OR APPLICATION NUMBER: 60/146,222
OR FILING DATE: July 28, 1999
OR APPLICATION NUMBER: PCT/US98/19330
OR FILING DATE: September 16, 1998
OR APPLICATION NUMBER: PCT/US98/25108
OR FILING DATE: December 1, 1998
OR APPLICATION NUMBER: 09/216,021
OR APPLICATION NUMBER: 09/216,021
                                                     OR FILING DATE: December 16, 1998
OR APPLICATION NUMBER: 09/218,517
OR FILING DATE: December 22, 1998
OR APPLICATION NUMBER: 09/254,311
OR FILING DATE: March 3, 1999
OR APPLICATION NUMBER: PCT/US99/12252
OR FILING DATE: June 22, 1999
OR APPLICATION NUMBER: PCT/US99/21090
OR FILING DATE: September 15, 1999
OR APPLICATION NUMBER: PCT/US99/28409
OR FILING DATE: NO. US20020173463Alember 30
OR APPLICATION NUMBER: PCT/US99/28313
OR APPLICATION NUMBER: PCT/US99/28313
OR APPLICATION NUMBER: NO. US20020173463Alember 30
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IOR FILING DATE: December 16, 1997
IOR APPLICATION NUMBER: 60/069,702
IOR FILING DATE: December 16, 1997
IOR APPLICATION NUMBER: 60/069,870
IOR FILING DATE: December 17, 1997
IOR APPLICATION NUMBER: 60/069,873
IOR FILING DATE: December 17, 1997
IOR APPLICATION NUMBER: 60/069,017
IOR APPLICATION NUMBER: 60/070,440
IOR FILING DATE: December 18, 1997
IOR APPLICATION NUMBER: 60/074,086
IOR APPLICATION NUMBER: 60/074,086
IOR APPLICATION NUMBER: 60/074,086
IOR APPLICATION NUMBER: 60/074,092
IOR FILING DATE: February 9, 1998
IOR APPLICATION NUMBER: 60/074,092
IOR FILING DATE: February 9, 1998
IOR APPLICATION NUMBER: 60/074,092
IOR FILING DATE: February 25, 1998
IOR APPLICATION NUMBER: 60/112,850
IOR APPLICATION NUMBER: 60/113,296
IOR APPLICATION NU
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; ORGANISM: HOMO
US-09-944-944-41
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LENGTH: 1377
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Best Local Similarity 100.0%;
Matches 1377; Conservative (
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IOR APPLICATION NUMBER: PCT/US99/30095
IOR FILING DATE: December 16, 1999
IOR APPLICATION NUMBER: PCT/US00/03565
IOR FILING DATE: February 11, 2000
IOR APPLICATION NUMBER: PCT/US00/04414
IOR FILING DATE: February 22, 2000
IOR APPLICATION NUMBER: PCT/US00/05841
IOR FILING DATE: March 2, 2000
IOR APPLICATION NUMBER: PCT/US00/08439
IOR FILING DATE: March 30, 2000
IOR APPLICATION NUMBER: PCT/US00/14042
IOR FILING DATE: May 2, 2000
IOR APPLICATION NUMBER: PCT/US00/2071
IOR FILING DATE: July 28, 2000
IOR APPLICATION NUMBER: PCT/US00/32678
IOR FILING DATE: July 28, 2000
IOR APPLICATION NUMBER: PCT/US00/32678
IOR FILING DATE: December 1, 2000
IOR APPLICATION NUMBER: PCT/US00/32678
IOR FILING DATE: December 1, 2000
IOR APPLICATION NUMBER: PCT/US00/32678
IOR FILING DATE: FEBRUARY 28, 2001
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CGACCGCGTGCTGGTGAACGAGCAGGGACATTACGACGCCGTCACCGGCAAGTTCACCTG
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Pred. No. 0;
0; Mismatches
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RESULT 5
US-09-944-907-41
           GENERAL INFORMATION:

APPLICANT: Baker, Key
APPLICANT: Botstein,
APPLICANT: Beton, Dan
APPLICANT: Eaton, Dan
APPLICANT: Errara, N
APPLICANT: Ferrara, N
APPLICANT: Goddard, A
APPLICANT: Goddwski,
APPLICANT: Gorney, Au
APPLICANT: Gurney, Au
APPLICANT: Hilan, Ke
APPLICANT: Napier, Ma
APPLICANT: Napier, Ma
APPLICANT: Napier, Ma
APPLICANT: Tumas, Dan
APPLICANT: Wood, Will
TITLE OF INVENTION: S
TITLE OF INVENTION:
                                                                                                                                                                                    Sequence 41, Application US/09944907 Publication No. US20020198147A1
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         INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES INVENTION: ACIDS ENCODING THE SAME
                              Roy, Margaret
Tumas, Daniel
Wood, William
                                                                                                                                                                                                                                      GTGTAAGTCCCCCAGTTGCTCTGGTCCAGGAGCCCACGGTGGGGTGCTCTCTTCCTGGTC
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                                                                                 Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
                                                                                                            Gerritsen, Mary
Goddard, Audrey
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                                                        Kljavin, Ivar
Napier, Mary
                                                                          Hillan, Kenneth
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                  AND
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CURRENT APPLICATION NUMBER: US/09/944,9
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 41
LENGTH: 1377
TYPE: DNA
ORGANISM: Homo Sapien
US-09-944-907-41
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Best Local Similarity
Matches 1377; Conserv
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CGACCGCGTGCTGGTGAACGAGCAGGGACATTACGACGCGGTCACCGGGCAAGTTCACCTG
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Pred. No. 0;
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Sequence 41, Application US/09944929

Publication No. US20020197612A1

GENERAL IMFORMATION:
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Eaton, David
APPLICANT: Elivaroff, Ellen
APPLICANT: Elivaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Christopher
APPLICANT: Grimaldi, Christopher
APPLICANT: Hillan, Kenneth
APPLICANT: Hillan, Kenneth
APPLICANT: Nayler, Mary
APPLICANT: Nayler, Mary
APPLICANT: Nayler, Mary
APPLICANT: Noy, Margaret
APPLICANT: Noy, Margaret
APPLICANT: Wood, Milliam
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
ITILE OF INVENTION: ACIDS ENCODING THE SAME
ITILE OF INVENTION: ACIDS ENCODING THE SAME
ITILE OF INVENTION: NUMBER: US/09/944,929
CURRENT APPLICATION NUMBER: US/09/944,929
CURRENT FILLING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
TYPE: DNA
OFFICIAL DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
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US-09-944-929-41
                                       TYPE: DNA
ORGANISM: Homo
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GGTCATCCAGGAGGGCTGGCCCCCCTGGAATATTGTGAATGACTAGGGAGGTGGGGTAGA
                                   GCCCAAGCCAGCCTCGCTCTCGGGGGGGGGCCATGGTGAGGCTGAGGCTGAGGACCAAGT
                                                                                                              CCAGGTGCCTGGGGTCTACTACTTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCA
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FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/028,072

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/049911

PRIOR PILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/056974

PRIOR FILING DATE: 1997-09-26

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059115

PRIOR PILING DATE: 1997-09-17

PRIOR PILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/05912

PRIOR PILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/05912

PRIOR FILING DATE: 1997-09-17

PRIOR PILING DATE: 1997-09-17

PRIOR PILING DATE: 1997-09-17

PRIOR PILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/05935

PRIOR PILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/05935

PRIOR PILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/059368

PRIOR PILING DATE: 1997-09-19

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Watanabe, Colin K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sherwood, Steven Smith, Victoria
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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b. US20030004311A1
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OR FILING DATE: 1997-12-16
OR APPLICATION NUMBER: 60/072320
OR FILING DATE: 1998-01-23
OR APPLICATION NUMBER: 60/073612
OR FILING DATE: 1998-02-04
OR APPLICATION NUMBER: 60/074086
OR APPLICATION NUMBER: 60/074086
OR APPLICATION NUMBER: 60/074086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DR APPLICATION NUMBER: 60/065186
DR FILING DATE: 1997-11-12
DR APPLICATION NUMBER: 60/065846
DR FILING DATE: 1997-11-17
R APPLICATION NUMBER: 60/066364
DR FILING DATE: 1997-11-21
DR APPLICATION NUMBER: 60/066453
DR FILING DATE: 1997-11-24
DR APPLICATION NUMBER: 60/066511
DR FILING DATE: 1997-11-24
DR APPLICATION NUMBER: 60/066770
DR FILING DATE: 1997-11-24
DR APPLICATION NUMBER: 60/069212
DR FILING DATE: 1997-12-11
DR FILING DATE: 1997-12-11
DR APPLICATION NUMBER: 60/069218
DR APPLICATION NUMBER: 60/069278
DR APPLICATION NUMBER: 60/069278
DR APPLICATION NUMBER: 60/069334
DR APPLICATION NUMBER: 60/069334
DR FILING DATE: 1997-12-11
DR APPLICATION NUMBER: 60/06934
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DR FILING DATE: 1997-10-29

DR APPLICATION NUMBER: 60/063738

DR FILING DATE: 1997-10-29

DR APPLICATION NUMBER: 60/063755

DR FILING DATE: 1997-10-17

DR APPLICATION NUMBER: 60/064248

DR APPLICATION NUMBER: 60/064248

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DR FILING DATE: 1997-11-07
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DR FILING DATE: 1997-10-28
DR APPLICATION NUMBER: 60/063704
DR FILING DATE: 1997-10-29
DR APPLICATION NUMBER: 60/063733
DR FILING DATE: 1997-10-29
DR FILING DATE: 1997-10-29
                                                                                                              APPLICATION NUMBER: 60/078910 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/079294
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FILING DATE: 1997-10-27
APPLICATION NUMBER: 60/063550
FILING DATE: 1997-10-28
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FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/063327
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APPLICATION NUMBER: 60/06287
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                                   FILING DATE: 1998-03-25
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FILING DATE: 1998-02-27
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APPLICATION NUMBER: 60/091519
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OR APPLICATION NUMBER: 60/084600
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084627
OR APPLICATION NUMBER: 60/084637
OR APPLICATION NUMBER: 60/0854637
OR APPLICATION NUMBER: 60/085149
OR FILING DATE: 1998-05-12
OR APPLICATION NUMBER: 60/085323
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085338
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085339
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085379
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085697
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085704
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085704
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085704
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/086414
OR FILING DATE: 1998-05-22

DR FILING DATE: 1998-04-15

PR APPLICATION NUMBER: 60/081818

DR FILING DATE: 1998-04-15

PR APPLICATION NUMBER: 60/082999

DR FILING DATE: 1998-04-24

DR APPLICATION NUMBER: 60/083322

DR FILING DATE: 1998-04-28

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1998-04-14

60/081817 60/081695 60/081229 APPLICATION NUMBER: APPLICATION NUMBER: 60 FILING DATE: 1998-03-3

60/080165 60/081203

OR AFPLICATION NUMBER: 60/088810
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/08858
OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/089532
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OR FILING DATE: 1998-06-18
OR APPLICATION NUMBER: 60/089907
OR FILING DATE: 1998-06-19
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OR APPLICATION NUMBER: 60/088026
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088730
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088741
OR FILING DATE: 1998-06-10

APPLICATION NUMBER: 60/ FILING DATE: 1998-05-22 APPLICATION NUMBER: 60/ FILING DATE: 1998-05-28

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APPLICANT: Beresini, Maureen
APPLICANT: Beresini, Maureen
APPLICANT: Beresini, Maureen
APPLICANT: Beresini, Maureen
APPLICANT: Deborge, Laura
APPLICANT: Deborge, Laura
APPLICANT: Gesnoyers, Luc
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddwaki, Paul J.
APPLICANT: Goddwaki, Paul J.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Shang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCI
FILE REFERENCE: P330RIC17
CURRENT APPLICATION NUMBER: US/10/121,049
Prior ADDICATE: 2002-04-12
                                                                                              Prior Application removed - Se SEQ ID NO 361 : LENGTH: 1377
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OY 241 CGTCCTGCTGCTCCTGGGCGGCTGGGGCGGCTCGCCCCACTGGACGACAACAACAACATCCC 300	Qy 181 GGGACTGCGAGAGGACCCCGGGCTCCGGGGCTGCCAGCGCTATGAGGCCACTCCT 240	Qy 121 CCAACTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGG 180	Qy 61 TGGGGTGACGGCAGGGCAGGGGCGCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCA 120	Qy 1 GACTAGTTCTTGGAGTCTGGGAGGAAGCGGAAGCGGAGGGAG	Query Match 100.0%; Score 1377; DB 9; Length 1377; Best Local Similarity 100.0%; Pred. No. 0; Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	TYPE: DNA ; ORGANISM: Homo Sapien US-10-123-904-361	Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550 SEQ ID NO 361 FENGRAL 1373	TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C54 CURRENT APPLICATION NUMBER: US/10/123,904		APPLICANT: Smith, Victoria APPLICANT: Smith, Victoria APPLICANT: Stewart, Timothy A.	APPLICANT: Godowski, Paul J.		Publication No. US20030022328A1  GENERAL INFORMATION: APPLICANT: Baker Kevin P. ADRICANT: Baker Kevin P.	)04-3	QY 1321 GATCACTCAATAAACCTAAGAACCCTCATAAAAAAAAAA	QY 1261 CTCTGCTTCTCTGGATCCTCCCCACCCCCTCCTGCTCCTGGGGCCGGCC	QY 1201 GTGTAAGTCCCCCAGTTGCTCTGGTCCAGGAGCCCACGGTGGGGTGCTCTCTTCCTGGTC 1260	Db 1141 GCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCAGAGGAGTGTGCTGTGCTAGAA 1200
Qy Db	Oy Db	Qy Db	Qy Db	Qy	Qy	Qy	Qy	Qy Db	Oy Db	Oy Db	Oy Db	. Qy	Qy	Qy Db	ДУ	Qy Db	Qy Db	Db
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APPLICANT: Wood, William
APPLICANT: APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 361
LENGTH: 1377
TYPE: DNA
ORGANISM: Homo Saplen
US-10-140-470-361
100.0%: Score 1377; DB 9; Length 130.0%: Scor
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Publication No. US20030022331A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Desorge, Laura
APPLICANT: Desorge, Laura
APPLICANT: Desorge, Laura
APPLICANT: Filvaroff, Ellen
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US-10-140-470-361
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Best Local Similarity 100.0%;
Matches 1377; Conservative 0
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Desnoyers, Luc
Filvaroff, Ellen
Gao, Wel-Olang
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Sequence 361, Application
Publication No. US2003002:
GENERAL INFORMATION:
APPLICANT: Baker, Kevin p
APPLICANT: Beresini, Mau
APPLICANT: Desnoyers, Luur
APPLICANT: Tilvaroff, Eli
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mai
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US-10-175-746-361
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Filvaroff, Ellen
Gao, Wei-Qiang
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                                                             Beresini, Maureen
DeForge, Laura
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: LENGTH: 1377

: TYPE: DNA

: ORGANISM: Homo Sapien

US-10-175-746-361
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CURRENT FILING DATE: 2002-06-19
PLOT APPLICATION removed - See File Wrapp
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 361
LENGTH: 1377
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Best Local Similarity 100.
Matches 1377; Conservative
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APPLICANT:
APPLICANT:
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   CCAGGTGCCTGGGGTCTACTACTTCGCCGTCCATGCCACCGTCTACCGGGGCCAGCCTGCA
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A
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Wood, William
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APPLICANT:
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    APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C382
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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                                              Wood, William
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                                                                          Stewart, Timothy A
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                                                                                                                                                                             DeForge, Laura
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NUMBER: US/10/176,918
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CURRENT FILING DATE: 2
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NUMBER OF SEQ ID NOS: 5
SEQ ID NO 361
LENGTH: 1377
TYPE: DNA
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; LENGTH: 1377
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US-10-176-921-361
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Query Match
Best Local Similarity
Matches 1377; Conserv
                                                                                                    Prior Application removed
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 361
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 361, Publication No
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 9330R1C288
CURRENT APPLICATION NUMBER: US/10/176,921
CURRENT FILING DATE: 2002-06-20
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith Victoria
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No. US20030027276A1
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Desnoyers, Luc
Filvaroff, Ellen
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Gerritsen, Mary E.
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    Conservative
              100.0%;
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              Score 1377;
Pred. No. 0;
  Mismatches
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; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Homo :
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APPLICANT:
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Best Local Similarity
Matches 1377; Conserv
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C154
CURRENT APPLICATION NUMBER: U$\( \)2,10/137,865
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wr.
NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 361, Appropriate Publication No.
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Watanabe, Colin K
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Filvaroff, Ellen
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Conservative 0
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CITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCL
FILE REFERENCE: P3330R10162
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Filvaroff, Ellen
Gao, Wei-Qiang
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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DeForge, Laura
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